

GenCore version 5.1.3
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om nucleic - nucleic search, using sw model

Run on: october 22, 2002, 08:46:06 ; Search time 3976 Seconds
(without alignments)
17294,919 Million cell updates/sec

Title: US-09-904-389-1
Perfect score: 3286
Sequence: 1 attcattatcaggaaagaa.....aaaaaaaaaaaaaaaaaaaa 3286

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: GenEmbl:

- 1: qb_ba:*
- 2: qb_htq:*
- 3: qb_in:*
- 4: qb_om:*
- 5: qb_ov:*
- 6: qb_pat:*
- 7: qb_ph:*
- 8: qb_pl:*
- 9: qb_pr:*
- 10: qb_ro:*
- 11: qb_sts:*
- 12: qb_sy:*
- 13: qb_un:*
- 14: qb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mn:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htq_hum:*
- 31: em_htq_inv:*
- 32: em_htq_other:*
- 33: em_htqo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	ID	Description

1	1195.6	36.4	3121	8	AY032953	AY032953
2	996.8	30.3	2829	8	AF096250	AF096250
3	996.8	30.3	2917	8	LE1YRKINA	LE1YRKINA
4	979.2	29.8	2836	8	AF110518	AF110518
5	898.8	27.4	3033	6	114046	114046
6	898.8	27.4	3033	6	135764	135764
7	898.8	27.4	3033	8	ATHCTR1A	ATHCTR1A
8	856.6	26.1	2767	8	AF110519	AF110519
9	439.4	13.4	1795	8	AF386508	AF386508
10	342.8	10.4	3158	8	AF305911	AF305911
11	340.6	10.4	3338	8	AF305912	AF305912
12	339.4	10.3	3456	8	LEAJ5077	LEAJ5077
13	323.2	9.8	3081	8	AF305913	AF305913
14	311.4	9.5	633	8	AF247567	AF247567
15	308.2	9.4	1521	8	ATY14199	ATY14199
16	283.2	8.6	681	8	AY029067	AY029067
17	270.2	8.2	2392	8	AY062764	AY062764
18	270.2	8.2	2824	8	AY056257	AY056257
19	267.8	8.1	2923	8	AY074498	AY074498
20	260.8	7.9	564	8	AF261147	AF261147
21	242.8	7.1	2837	8	AY059769	AY059769
22	208	6.3	339	8	AF387794	AF387794
23	158.4	4.8	348	8	AF261148	AF261148
24	156.2	4.8	3181	8	AY049228	AY049228
25	155.2	4.7	6295	6	114048	114048
26	155.2	4.7	6295	6	135766	135766
27	155.2	4.7	6312	6	114049	114049
28	155.2	4.7	6312	6	114050	114050
29	155.2	4.7	6312	6	114051	114051
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36	155.2	4.7	2122	8	AY070086	AY070086
37	125.8	3.8	1610	8	PSY298992	PSY298992
38	122	3.7	1584	3	DD1297966	DD1297966
39	118.2	3.6	1724	8	SOYPROKIN	SOYPROKIN
40	106	3.2	2280	8	AY062096	AY062096
41	105	3.2	2271	8	AF462860	AF462860
42	103.4	3.1	2271	8	AF271206	AF271206
43	101.4	3.1	561	8	AF271206	AF271206
44	100.4	3.1	1168	8	AY063013	AY063013
45	100.4	3.1	2108	8	AY035004	AY035004

ALIGNMENTS

RESULT 1	AY032953	3121 bp	adna	cloned	11 NOV 2002
AY032953	Rosa hybrid cultivar	cpcl-like protein kinase (cpcl)	mbNA	cloned	
LOCUS	AY032953				
DEFINITION	AY032953				
ACCESSION	AY032953				
VERSION	AY032953.1	GI:13936370			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
Source					
Location/Qualifiers					
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/db_xref="taxon:128735"					

LOCUS LETYRKINA 2917 bp mRNA linear PLN 02 SEP 1997
DEFINITION Lycopersicon esculentum mRNA for putative protein kinase.
ACCESSION Y13273
VERSION Y13273.1 GI:2370252
KEYWORDS protein kinase;
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 2917)
AUTHORS Wang, Y. and Li, N.
TITLE A cDNA sequence isolated from the ripening tomato fruit encodes a
putative protein kinase.
JOURNAL Plant Physiol. 114, 1135-1135 (1997)
REFERENCE 2 (bases 1 to 2917)
AUTHORS Wang, Y.
TITLE Direct Submission
JOURNAL Submitted (19 MAY 1997) Y. Wang, The Hong Kong Univ. of Sci. and
Tech., Biology Department, Clear Water Bay, Kowloon, HONG KONG
FEATURES
source location/Qualifiers
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STASAVTMSHRLWINGMAYEDKVPDGFYIYMCPYVVALCQSVQSGPFPSPFIR
AVDSPKASVEVILLIDRCNDLSLKELQNRIHSISPSCITTKAEVDQLAKLVCDHMGA
APAGEEELVSMKSGCSNDIKDEFTIVLPIGLSVTCPIPALIFKVIADILDTPTI
AKGCKYCNSSDASSCLVRPHDREYLVDLGKPGVLSEPPSLNGPSSIIPSPIRFPP
RYQVEPTTFRESLAQETLESNLIEFDSSACAAGAQAQSDERSCIDFNNVVSF
SSNRDEISQLPLPENAWKCKDKESOLSKMYNPENLNVMDEDQVLVKHVPPFE
DAQSPMTIRDVNDTRFLAGGHVVSAIPSEELDLDVEENLTPWNDLILMEKIGAGSF
CTVHRGDWHGSDVAVKILMFQDFHAERLKEFLREVAIMKRLRHPNIVLFMGAVIQPPN
LSIVTEYLRSGLYRLLHKPGAPEVIDERRPRLCMAYDVANGMNYLHKRNFFIVHEELK
SPNLLVDKAYIVKICDFGRPKANTFLSSKTAAGTPEWMAFEVIRDEFSNEKSDVIS
FGVILWEIALIQQPWNKLNFQVIAAGFENFKRLDIPSLNPQVAIIIFACWANETPW
RPSFSTIMDLRPHLKSPLPPPCHTDMQLLS"
BASE COUNT 771 a 572 c 700 q 874 t
ORIGIN
Query Match 30.3%; Score 996.8; DB 8; length 2917;
Best local Similarity 67.8%; Pred. No. 9.5e-234;
Matches 1512; Conservative 0; Mismatches 679; Indels 39; Gaps 7;
QQ 477 TTCCGAGCTGATGAAGCTGIGGGAAGTGGAGGTTCGTCTGGAAGAGAGCTGGGCCAGCA 536
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DB 402 TTCCTTGAGCATAAAGATGAGGCTGTGGCTGGCTGGCAAGGAGCTGGGCCAGCA 461
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QQ 537 GAGGGAAGAGAGCTTTCAGTTGCACAGCCCTTGGTTCTTAGGCTTCTTCAGATGNAC 596
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DB 462 GAGGGAAGAGAGTTATCAGTCGACGTAGCTTGGCAATAAGGCTCTCTTCAGAGCAAC 521
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QQ 597 TTGCGCGATGATCCCAACTTATGATCCGATTCCAGACGAGCCAGCTTTAAGATCGTT 656
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DB 522 CTGCGATGATGATCCCAACTTCTTGATCTCTGACTGATGATTGCGATCCCGAGATTC 581
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QQ 657 A-----TCGATTTTCAGCTGAGGCCAICTGGCATCGGTTCTGGGTAAATGGATGATGC 710
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DB 582 AGATTCTACTGCAFCAGGUGTAACAAATCTCACATCCGATTGTGGATAAATGCATGTATGC 641

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QY	1608	TTGAAAAGTCTGAGCAAAATTAGAAATCAATGCTTGGTTCTCTCCATAATAGTGTACAGTTCGACCCG	1666
DB	1413	AGATAAAGAAATCTCAACCTTCTAANAATGTATAAATCTCTGAAGTAATGTTAAACCCAGTGAA	1472
QY	1668	TTTTCGTAGAAAAATGTAAGTGGCTTTAAGCCATAATCTACACACATTTGGTTCTGAAGATTCGGA	1727
DB	1473	CAAGGACGAGGACGAGGTTCCTTGTGAAGCAATGCTCTCCATTCGCGGAAGATGC-----	1526
QY	1728	GCATCTCTTAGCAATTGCTTCATCCCAAGGATGGATCATGTTAACAAATTTACCATTTGTTC	1787
DB	1527	---TCAATCACCGATACACACGACACAGATACAGTAATAATGATACACTAGCTTCTTCTGCTGGAGC	1583
QY	1788	TGGTAGTCAGTTGCAATTAGAAAAACAA---ATGAGCTTTCCCTTGGCTTAGAAAGATTTGGT	1844
DB	1584	AGGTCATGTTGTTCTTGCTATACCAAGTGAAAJAACTTGATCTCGATCTTAGAAAGAGTTCA	1643
QY	1845	TATTCCATGGACAGATCTGATTTGATTTGAGGGCAGAAAAATGGAGACATCTTCTTTTCCCACTGT	1904
DB	1644	TATTCCATGGAAATGATCTGGTTCTAATGGAGAAAAATGGGGCAGGCTCTTTTGGTACTGT	1703
QY	1905	ATATGCTGTGACTGGCATGGCTCTGATGTCTGCTGTGAAGATCTCTACAGAACACAAGACTT	1964
DB	1704	TCACCTGGGTGATTGGCATGGCTCTGATGTCTGGCTGAGATCTCTCATGCAACACATTT	1763
QY	1965	CCATCTGTAAACCTGCTTAAATGATTTCTTCAGACAGAGTTGCTATCATCAAAATCTTTACCAACA	2024
DB	1764	TCATTCACAGCGACTCAAGGAATTTTTGAGGGAGGTTGCCAATTATGAAAGGGTTTGGACA	1823
QY	2025	TGCTAATATTGTACTGTTTATGGGTGGCTGACCAAGCCACCAAAACTTGTCCATTTGTAC	2084
DB	1824	TCATAAATTCTACTTTTATGGGTGCTGATTCAGCCACGCAAAATTTGTCCATAGTCAAC	1883
QY	2085	CGAATATCTATCCAGAGGTAGCTTCTATAAGCTTTTGCATAAAGTCAGGTG---TCAAGA	2141
DB	1884	CGAATATTATCCAGAGGTAGCTTATAAGACTTCTCATAAACCTTGGTGGCAAAAAAGT	1943
QY	2142	CATAGATCAAAACAGTCCGAATAAAATATGGCTTTTGATCTGGCCAAAGCGAATGAACCTACCT	2201
DB	1944	GTTCGATGAAGAGCTCCCTCTGCTTTGGCTTAGGATGTGGCGAATGGCATCAATTATCT	2003
QY	2202	CAACACAGCTGATCTCCCAATTGTCTATCTGTGATTAAAAATCACCCCAATCTGTTAGTTGA	2261
DB	2004	TCACAAAGCCAAATCTCCCATTTGTGACCCGAGATTAAAAATCCCAAAATCTCTTAGTAGA	2063
QY	2262	CAAGAAGATATACAGTCAAGTTTCTGATTTTGGTCTCTGCCGTTAAAGGCACGACACATT	2321
DB	2064	CAAAAAATATACAGTCAAGATCTGTGATTTTGGCTTTCTCGTTCTCAACCCCAACACATT	2123
QY	2322	TCTTTCATCCAAATCTGCACCTGGCAACACATGAAATGGATGGCACCCAGAGTACTACCGGA	2381
DB	2124	CTTTCTCATCAAGACCTGCTCTGGGAATCGGGAATCGATGGCGCTGAAGTTATTCTGTGA	2183
QY	2382	TGAACCATCAAAATGAAAAGTCAGATGTTTACAGCTTTTGGAGTGAATTTGTGGGAGTTGGC	2441
DB	2184	TGAACCATCAAAATGAGAAAATCTGATGATATACAGCTTTGGTGTCTATTTTGTGGGAGCTGGC	2243
QY	2442	AACCTTGCACACAGCATGTGTGTAATCTTAAAGCCAGCTCAGGTTCTCGCACTTGTGTGGATT	2501
DB	2244	AACCTCTCAACAACCAATGGAAATAAATTGAAGCCAGCCACAGGTTATAGCAGCTGTGGGCTT	2302
QY	2502	TAAAGGCAAAAGGCTTGACATCCCAAGTGAATGTAATCCCAAAATGGCTTCTCTTAATAGT	2561
DB	2304	TAAACAGAAACAGCTTGATATTCTCAAGTGTCTTCAATCTCTCACTTCTGGATTATTATGA	2362
QY	2562	GGCTTCTTGGGGGATGAGCAATGGAAGTTCCTTCTTTTCCAGCATTAATGSAAAACCTT	2621
DB	2364	AGCTTCTTGGGCTAAATGAGGCTGGAAGGCTGGCTTCTTCTCACTATCATCGATATGCT	2423
QY	2622	GAAGCAANTGACTAAACAAGGGGCAAGCTCAACAAAGTGGCACAGACACACCTTCTCGTTAT	2681
DB	2424	CAGAGCTCATCTTAAATCTCTCTACCTCCACGAGTCTCACACAGACATGCGACTTCTCTCTC	2482

QY	2682	GTGACAAATCTGTG	2694
Db	2484	ATGAATAACCTGTG	2496
RESULT 9			
AF386508			
LOCUS			
DEFINITION	Pyrus communis putative serine/threonine-specific protein kinase (CTRL) mRNA, partial cds.		
ACCESSION	AF386508		
VERSION	AF386508.1 GI:18252316		
KEYWORDS			
SOURCE	pear.		
ORGANISM	Pyrus communis		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus;		
REFERENCE	1 (bases 1 to 1795)		
AUTHORS	El Sharkawy,I., Li,Z.G., Latche,A. and Leclercq,J.M.		
TITLE	Ripening related genes in pear (Pyrus communis)		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1795)		
AUTHORS	El Sharkawy,I., Li,Z.G., Latche,A. and Leclercq,J.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-MAY-2001) Biologie Molculaire et Physiologique des Maturation des Fruits, INP - ENSAI, Av. de l'Aurore, 43126, France Castanet Tolosan Cedex		
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CDS	c1..1565		
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	/codon_start 5		
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	/protein_id="AAL66190.1"		
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BASE COUNT	482 a	359 c	436 q
ORIGIN	518 t		
Query Match			
Best Local Similarity 68.9%; Score 439.4; DB R; Length 1795			
Matches 619; Conservative 0; Mismatches 276; Indels 0; Gaps 19			
QY	1915	TCAGCTTTCACTGCCTTAGACAGATTGGTATATCAAGAAAGAAATTAAGAAGAAATGA	1929
Db	692	TCAACCGAATTTCGAATGACGCTTTTACAATTCATAGAAATAGTAAATGAAATGAAA	704
QY	1875	GAAAAATTGAAAGAGGACCTCAGAGAAACAAGATLLCCATCTTGAGGCTGATGAGAG	1904
Db	752	GGTGGTCTCATGCTGATTCATCTGGACACGATGATGATGCTGAAAGAAATGAAATG	811
QY	1935	TGCTGTGAAAGATGCTCACAGAAACAAGATLLCCATCTTGAGGCTGATGAGAGAG	1964
Db	812	TGCTGTGAAAGTCTCAACCGTTCAGGATTCATGATGATGATGAAATGAAAGATTTTT	861
QY	1995	AGACGTTGGTATCATGAAATCTTTACAGAAATCAATTAATATGTAATGTAATGAGG	2064


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QY 2374 CTACGGGATGAACGATCAAAATGAAAAGTCAGATGTTTACAGCTTTGGAGTGATTTGTGG 2433
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Db 914 TTGAGGAATGAACGGGCTAATGAGAAAATGAGAGCTTTACAGCTTTGGTGTCAATTTGG 973
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2434 GAGTGGCAACTTTGCAACAGCCATGGTGTAAATCTAAACCCAGCTCAGGTTGTGGAGCT 2493
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 974 GAATTAGCTACTTCAGGGCTCCCGTGGAAAGGTTTGAACCCGATGCAAGTCGTTGGAGCT 1033
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2494 GTTGGATTTAAAGGCCAAAAGGCTTGACATCCGACGTGATGTAAATCCCAAAFTGGGCTCC 2553
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1034 GTGGGATTCAGAAATCCAGGCTTGAAATCCGAGATGATCGATCTAACTGTGGCAGAG 1093
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2554 TTAATAGTGGCTTGGTGGGCGGATGAGGCAATGGAAACGTCCTTCTTTTCCAGCAATATG 2613
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1094 ATAATCCGTGAATGTGGCAACGGAAACCGCATTTACGGCCATCGTTTACACACAGCTGATG 1153
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2614 GAAACCTTGAAC 2626
  | | | | | | |
Db 1154 CAAAGTTGAAGC 1166
  | | | | | | |
```

Search completed: October 22, 2002, 09:53:16
Job time : 4007 secs



GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2002, 08:46:06, Search time 347 Seconds
(without alignments)
16258.734 Million cell updates/sec

Title: US-09-904-389-1
Perfect score: 3286
Sequence: 1 attcattatccqqaacaga.....aaaaaaaaaaaaaaaaaaaaa 3286

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database				N_Geneseq_032802.*	
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22:	US1051	Arabidopsis thaliana	gus1	gus1	gus1
23:	US1051	Arabidopsis thaliana	gus1	gus1	gus1
24:	US1051	Arabidopsis thaliana	gus1	gus1	gus1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query *		DB ID	Description
		Match	Length		
1	900.4	27.4	2890	15	AAQ57911 Arabidopsis thaliana
2	898.8	27.4	3033	16	AAQ98816 Arabidopsis thaliana
3	898.8	27.4	3033	18	AAI67126 Constitutive tripl
4	442.8	10.4	3160	22	AAC90485 Rice EDRI cDNA, O
5	340.6	10.4	3316	22	AAC90486 Barley EDRI cDNA
6	323.2	9.8	3081	22	AAC90484 Arabidopsis thaliana
7	155.2	4.7	5873	15	AAQ57913 Arabidopsis thaliana
8	155.2	4.7	5890	15	AAQ57912 Arabidopsis thaliana
9	155.2	4.7	5890	15	AAQ57914 Arabidopsis thaliana

10	155.2	4.7	5890	15	AAQ57915 Arabidopsis thaliana
11	155.2	4.7	6295	16	AAQ98818 Arabidopsis thaliana
12	155.2	4.7	6295	18	AAI67128 Constitutive tripl
13	155.2	4.7	6312	16	AAQ98817 Arabidopsis thaliana
14	155.2	4.7	6312	16	AAQ98819 Arabidopsis thaliana
15	155.2	4.7	6312	16	AAQ98820 Arabidopsis thaliana
16	155.2	4.7	6312	16	AAQ98821 Arabidopsis thaliana
17	155.2	4.7	6312	18	AAI67127 Constitutive tripl
18	155.2	4.7	6312	18	AAI67131 Constitutive tripl
19	155.2	4.7	6312	18	AAI67129 Constitutive tripl
20	155.2	4.7	6312	18	AAI67130 Constitutive tripl
21	126.2	3.9	2293	21	AAC48526 Arabidopsis thaliana
22	110.2	3.4	1631	21	AAC39537 Arabidopsis thaliana
23	94.1	2.9	1224	21	AAC4254 Arabidopsis thaliana
24	94.2	2.6	1063	22	AAH3476 Human colon cancer
25	92.8	2.5	2272	21	AAQ99736 Cardiovascular sys
26	91.6	2.5	1365	21	AAQ99727 cDNA encoding huma
27	91.6	2.5	1706	21	AAQ99726 cDNA encoding huma
28	91.6	2.5	2120	21	AAQ99726 cDNA encoding huma
29	91.6	2.5	2191	22	AAH99263 Human protein enzy
30	91.6	2.5	2194	21	AAQ99734 Cardiovascular sys
31	91.6	2.5	2220	21	AAQ99783 Human survival res
32	91.6	2.5	2403	22	AAI44791 Novel protein kind
33	91.6	2.5	2622	22	AAI75226 Human TGF beta rec
34	91.6	2.5	3967	22	AAH73366 Human cervical can
35	81.2	2.5	2254	21	AAQ99735 Cardiovascular sys
36	81	2.5	4515	23	ABL07083 Prosopha melanoid
37	80	2.4	2069	21	AAQ99737 Cardiovascular sys
38	77.4	2.4	1514	21	AAC47638 Arabidopsis thaliana
39	74.2	2.3	1947	13	AAQ23459 Human c-raf 1 gene
40	74.2	2.3	4835	23	AAQ63410 cDNA encoding novel
41	73.8	2.2	3981	18	AAI12154 Prosopha vitilis
42	73.8	2.2	1947	18	AAI18699 Human c-raf 1 gene
43	73.6	2.2	1947	20	AAQ33225 Human c-raf 1 gene
44	73.6	2.2	2004	22	AAI75129 cDNA encoding thio
45	73.6	2.2	2977	17	AAT30085 Human Raf-1 kinase

ALIGNMENTS

RESULT 1

AAQ57911

11 AAQ57911 standard, cDNA, 2890 bp.

XX AAQ57911;

AC AAQ57911;

XX US-09-904 (first entry)

XX Arabidopsis thaliana constitutive tripl response cDNA.

XX Constitutive tripl response gene, cDNA, ethylene phenotype

XX Plant hormone, stress response, constitutive mutant

XX Raf-1 kinase, threonine kinase, raf family, transmembrane protein, SS.

XX Arabidopsis thaliana.

XX Key location/Qualifiers

XX CDS 118..2583

XX /*taq= a

XX /product= CTRL

XX /note= "putative kinase"

PN WO9403047-A.

XX 17-FEB-1994.

XX 05-AUG-1993; 93WO-US07347.

XX 10-AUG-1992; 92US-0928464.

XX (TYPE-) UNIV PENNSYLVANIA.


```
QY 2008 ATGAAATGCTTTAGGACATGCTTAAATATGTTACATGTTTATGGGTCGGTGACAAAGCCACCA 2067
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 1915 ATGAAAGCCCTTCGCCACGCTAACATGTTCTCTTCATGGTGGCGGTGACATCAAGCTGCA 1974
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 2068 AACTTGTCATGTCACCGGAATATCTATGAGAGAGGTAGCTTGTATAGGCTTTTGCATAAG 2127
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Db 1975 AATTGTCAATAGTGACAGAATAATTGTCAAGAGGTAGTTTATACAGAGCTTTTGCATAAA 2034
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QY 2128 TCAGCTCTCA AAGACAATAGATGAAGACAGCTGCAATAAATATGCTTTTTCATGAGGA 2184
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 2035 AGTGGAGCAAGGAGCAATATAGATGACAGACAGCTGCGCTGAGTATGCTTATGATCTGGCT 2094
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 2185 AAGCAATTAAGTACCTCCACAGAGCTGATGCTCCCAATTTGCTCATCTGCAATTAATAATCA 2244
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 2095 AAGCAATGAATATCTTCACAAATGCAATCTCCCAATTTGCTCATGATGATGATGATGATCT 2154
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QY 2245 CGCAATCTGTTAGTIGACAGAGATATACAGTCAAGGTTTCTGATTTTCTGCTCTCTCTCT 2304
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 2155 CCAAACTTATGTTGACAAAAAATATACAGTCAAGGTTTGTGATTTTGTCTCTCTCTCT 2214
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 2305 TTAAAGCCAGCCACATTTCTTCAATCCAAATCTGCAATCTGCAATCTGCAATCTGCAAT 2364
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 2215 TTGAAGCCAGCAAGTTTCTTCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCTGCA 2274
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 2365 CACAGAGTACTAGGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 2424
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 2275 CACAGAGTCTGCGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 2334
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 2425 ATTTGTGAGAGTGGCAAGCTTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2484
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 2335 ATCTGTGAGAGTGGCAAGCTTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2394
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QY 2485 GTCGAGAGCTGTTGGATTTAAGGCAAAAGGCTTGACATCCCAAGCTGATGTAATCCCAAA 2544
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Db 2395 GTAGCTGAGAGTGGCAAGCTTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2454
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 2545 TTGGCTTCTTAATAGTGGCTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 2604
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 2455 GTTCAGAGCATAATGAGAGAGTGTGTGGAGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2514
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 2605 AATATATATGAAAGCTTGAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2664
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 2515 ACTATAATAGAGCTTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2574
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 2665 GA 2666
    ||
Db 2575 GA 2576
```

RESULT 2

AAQ98816
ID AAQ98816 standard: cDNA; 3033 BP.

XX
AC AAQ98816;

DT 19-JAN-1996 (first entry)

XX Arabidopsis CIR1 cDNA.

DE
KW CIR1; constitutive triple response; transgenic plant; ethylene;
KW stress tolerance; crop improvement; ss.

OS Arabidopsis thaliana ecotype Columbia.

PH Key Location/Qualifiers
FT CDS 118..2583

FT /*tag= a

PN U55444166-A.

XX 22-AUG-1995.

PD
XX

PF 10-AUG-1992; 92US-0928464.
XX
PR 12-JAN-1993; 93US-0003311.
PR 10 AUG 1992; 92US 0928464.
XX
PA (OYPE-) UNIV PENNSYLVANIA.
XX
PI Ecker JR, Kieber JJ;
XX
DR WP1; 1995.302162/39.
DR P-PSDB; AAR80574.
XX
PT New constitutive triple response genes and mutants - isolated from
PT Arabidopsis thaliana, used to produce transgenic plants with
PT improved properties
XX
PS Claim 1; Column 21-28; 41pp; English.
XX
CC The CIR1 gene was mapped to an interval between 2 RFLPs in
CC chromosome 5 of A. thaliana and a chromosome walk in this area was
CC initiated using a YAC library. 2 Clones were isolated and used to
CC probe a cDNA library derived from polyA RNA from 3-day-old dark-
CC grown, ethylene treated A. thaliana seedlings. The cDNA for the
CC CIR1 gene is given in AAQ98816. Expression of the CIR1 gene in
CC transgenic plants results in a dominant ethylene insensitive
CC phenotype.

XX
SQ Sequence 3033 BP; 797 A; 605 C; 751 G; 880 T; 0 other;

Query Match 27.4%; Score 898.8; DB 16; Length 3033;
Best Local Similarity 64.3%; Pred. No. 6.9e-242;
Matches 1582; Conservative 0; Mismatches 654; Indels 216; Gaps 7;

QY 253 AAAGGAGACACCGATAGGCTTTTTCATGCGATCGGAGTGGTGAACAGATTAAGACAC 412
DE 283 ATAGGAGATTTTATTTGTAATTTAATTTTATTTTATTTTATTTTATTTTATTTTATTT 442
QY 313 CAGGCTATCGGATAGGAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 466
DB 343 CAACCGAATCGGCTTGGGAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 402
QY 367 ATTCGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
DE 403 ATTCGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 441
QY 427 AACCTCGACACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 469
DB 462 -TGGGGGCTTAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 519
QY 487 ATCAAAAGCTTGGGAAAGTGGAGCTTGG- - - - - 514
DB 520 GAATTTGCTTGTGCTGAGAGATTTTGAATATACAGATGAGATGAGATGAGATGAGATGAG 579
QY 514 TCTGGAAGAGCTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 567
DB 580 TCTCATCTGGAAGAGCTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 639
QY 568 TTGCTTTTATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 627
DB 640 TTGCTTTTATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 699
QY 628 ATTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 687
DB 700 GTACCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 759
QY 688 TTCTGGGTAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 747
DB 760 TTCTGGGTAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 819
QY 748 CATGGGATGGACCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807
DB 820 AATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 879

XX The present sequence is given in a specification relating to the ERL1
CC gene located on Arabidopsis thaliana chromosome 1 between markers
CC ATH1 and NCC1. The disruption of the ERL1 gene is associated with
CC enhanced resistance of a plant to plant pathogens or other
CC disease-causing agents. A mutated transgene comprising the ERL1 gene
CC mutated at residue 696 of the of kinase-encoding domain may be introduced
CC into the plant genome to reduce expression of ERL1. Alternatively, a
CC transgene that expresses part or all of an antisense strand of the ERL1
CC gene may be introduced. A transgene which expresses a sense strand of
CC the ERL1 gene may be introduced to produce fertile Arabidopsis thaliana
CC plants. Transgenic plants exhibiting the desirable phenotypes of
CC lack of ERL1 protein, ERL1 mRNA, or enhanced resistance to plant
CC pathogens can be used for plant breeding, or directly in agricultural or
CC horticultural applications. Plants containing one transgene may also be
CC crossed with plants containing a complementary transgene in order to
CC produce plants with enhanced or combined phenotypes. ERL1 nucleic acids
CC may be used as probes to detect the presence and/or expression of ERL1
CC genes and to identify related genes from other plant species, such
CC as the present sequence from barley.
XX
SQ Sequence 3316 BP; 933 A; 699 C; 831 G; 852 T; 1 other;

Query Match 10.4%; Score 340.6; DB 22; Length 3316;
Best Local Similarity 63.3%; Pred. No. 219e-81;
Matches 539; Conservative 0; Mismatches 309; Indels 5; Gaps 11

QY 1804 AGAAACCAAAATGAGCTTCCCTTGGCTTAGAAGATTTGGTTATTCATGTAAGATCTT 1863
DB 2062 AGTAAAGTTGATTTGGTGTGGATGAGTATCAGTAATGGGAAATCTTTGGGAAGATCTT 2121
QY 1864 GATTTGATGGAGAAATTTGGAGCAGGTTCTTTTGGGACGTGTAATGTTGAGTGGTAT 1923
DB 2122 GTAAATGATCAAGAAATTTGGCAATAGTTTCAATGAGAGAGTCAATGATGAGTAT 2181
QY 1924 GGCTCTGATGTTGCTGTGAAGATCTCTCAGCAAGAACAGCTTCCATCTGAAATGGTATA 1983
DB 2182 GCAACTGAAGTAGCTGTAAAGAAAGTTCTTGGATCAAGAGTCTCAAGGTCATGTTGGAG 2241
QY 1984 GAGTTCTGAGAGAGGTTGCTATCATGAAATCTTACGACATCTTAAATATGTAATCTT 2043
DB 2242 CAAATTCCTGTTGTAAGTGGGATTTATGGCTGGCTGCTGATCTTAAATATGTTCTT 2301
QY 2044 ATGGGTGGGTGACCAAGACCCACCAAACTTGTGTAATGTCAGCAAGAAATATTAATGAAG 2103
DB 2302 ATGCGCGTGGTAAATAGGCTTCCACACTTATCTATGTAATGTAATATTTTAAAGAGG 2361
QY 2104 AGCTTGATAGGCTTTTGCATAGTCAAGTCAAGTGTCAAGACATAGATGAAATAGTGAATA 2163
DB 2362 AGCTTATATAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2421
QY 2164 AATATGGCTTTTGTATGTCGCAAGGGAATGAACTAGTCTGACAGATGCTATGTAATCTT 2223
DB 2419 AAAATGGCTTTGATGTCGCAAGGGAATGAACTAGTCTGACAGATGCTATGTAATCTT 2478
QY 2224 GTTCATGCTGATTTAAATATCAGGGAATGCTGTAGTGTAGTGTAGTGTAGTGTAGTGT 2283
DB 2479 GTTCACCGGATCTAAATATCAGGGAATGCTGTAGTGTAGTGTAGTGTAGTGTAGTGT 2538
QY 2284 TGTGATTTTGTCTCTCCGTTTAAAGGACGACATTTCTTGTATGTAATCTTGTATGTA 2343
DB 2539 TGTGATTTTGTCTCTCCGTTTAAAGGACGACATTTCTTGTATGTAATCTTGTATGTA 2598
QY 2344 GCAACACCTTGAATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2403
DB 2599 GGGACCTCTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2658
QY 2404 GATGTTTACAGCTTTTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2463
DB 2659 GATATTTACAGCTTTTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2718
QY 2464 AATCTAAACCCAGCTCAGGTTTGTGCGACGCTGTTGGATTTAAAGGCAAAAAGCTG 2523
DB 2718 AATCTAAACCCAGCTCAGGTTTGTGCGACGCTGTTGGATTTAAAGGCAAAAAGCTG 2777

QY 2137 AAAGACATAGATGAAGACAGCTGCAATATAATATGCTTTTGTGATGTCGCAAGGAATGAAC 2196
DB 2139 CAA--ATIGACAGAGAGCTAGCAATTAATAATGCGCTTGTGATGTCGCAAGGAATGAAT 2195
QY 2167 TACCTCCACAGAGCTGATCTCTCAATTTGTTATGCTGATTTAAATACACCGAATCTGTTA 2256
DB 2166 TCCCTCCATATTTATGTTACCAACAAATTTGTTATGCTGATTTAAATACACCGAATCTG 2255
QY 2257 GTTCACAGAGAAATATACATCAAGTTTGTGATTTGCTCTCTCTCTCTCTCTCTCTCTCT 2316
DB 2256 GTTCACAGAAATATACATCAAGTTTGTGATTTGCTCTCTCTCTCTCTCTCTCTCTCT 2315
QY 2317 ACATTTCTTTCATCCAAATCTGCAGCTGGACACCTGGAATGGATGGCACCAGAGTACTA 2376
DB 2316 ACATTTCTTTCATCCAAATCTGCAGCTGGACACCTGGAATGGATGGCACCAGAGTACTA 2375
QY 2377 GCGGATGAACCATCAATTAAGAAAGTCAGATGTTTACAGCTTTTCCAGTGTATTTTGTGG 2436
DB 2376 GCGGATGAACCATCAATTAAGAAAGTCAGATGTTTACAGCTTTTCCAGTGTATTTTGTGG 2435
QY 2437 TTGGCAACCTTTGCAACAGGCAATGAGTGTAACTAAACCCAGCTCAGCTTGTGCGAGTGT 2496
DB 2436 TTAGCAACACTTAGATGGCATGGAAATGCAATTAATCCCAATGTAAGTTGTTGGGGCAGTC 2495
QY 2437 GGAATTAAGGCAAGAGGCTGACATGCGCAGCTGAATGTAATCCCAATTTGGCTTCCCTTA 2556
DB 2436 GGTTCACAGGACAGAGGCTGACATGCGCAGCTGAATGTAATCCCAATTTGGCTTCCCTTA 2555
QY 2557 ATAGTGGCTTGTGTCGCGCATGAGGCAATGGAAGAGGCTGCTCTCTCTCTCTCTCTCTCT 2616
DB 2556 ATATGGAATGCTGTCGCAAGAGGATGCAATTTGCGGCGCTGCTCTCTCTCTCTCTCTCT 2615
QY 2617 AGCTTGAACCAATGACTAATAACAGGCAAGGCTGCAACCTCAACA 2654
DB 2616 GCTTTGAGAGCTGTCCAAAGGCTAGTAACCGCTTCTCA 2653

RESULT 5
AAC90486
ID AAC90486 standard; cDNA; 3316 BP.
XX AAC90486;
AC AAC90486;
XX
DT 1 MAR 2001 (first entry)
XX
DE Barley ERL1 cDNA.
XX
XX Barley; ERL1; enhanced disease resistance; anti-fungal;
KW antibacterial; gene therapy; transgenic plant; pathogen; ss.
XX
OS Hordeum vulgare.
XX
PN W020071696-A1.
XX
PD 30-NOV-2000.
XX
PF 26-MAY-2000; 2000W0-US14718.
XX
XX 26-MAY-1999; 99US-0135895.
PR
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
XX Innes KW, Frye CA;
PI
XX WPI; 2001-025156/03.
DR P-PSDB; AAB50443.
XX
XX New gene ERL1 of Arabidopsis thaliana, the disruption of which enhances
PT disease resistance in plants, is useful for producing transgenic plants
PT and mutants having increased resistance to plant pathogens.
XX
PS Example 2; Page 84-85; 91pp; English.

XX OS Arabidopsis thaliana.

XX XX

XX Key Location/Qualifiers

FT mutation 2347..2348

FT /*tag= d

FT /note= "site of X-ray-generated deletion of

FT nucleotides 2348-2364 (GTCGCTTAATCTGTTT)

FT from wild-type ctr genomic sequence AAQ57912"

XX XX

XX W09403047-A.

XX XX

XX 17-FEB-1994.

XX XX

XX 05-AUG-1993; 93W0-US07347.

XX XX

XX 10-AUG-1992; 92US-0928464.

XX XX

XX (UYPE-) UNIV PENNSYLVANIA.

XX XX

XX Ecker JR, Kieber JJ;

XX XX

XX WP1; 1994 065280/06.

XX XX

XX Constitutive triple response genes and ctr mutants - exhibit

XX phenotype resulting from exposure to ethylene in wild type

XX plants; eq in response to stress

XX XX

XX Claim 4; Page 48-53; 69pp; English.

XX XX

XX A cDNA clone (AAQ57911) and a genomic clone (AAQ57912) coding for the

XX wild-type constitutive triple response (CTR) gene in plants have

XX been isolated. The ctr gene encodes a protein resembling the Raf

XX family of serine/ threonine kinases. The ctrl-2 mutation (AAQ57913)

XX has a 17bp deletion from nucleotide 2348 to 2364 of the CTR genomic

XX DNA sequence. The mutation was generated by X-ray mutagenesis and

XX results in a constitutive "ethylene" phenotype.

XX XX

XX Sequence 5873 BP; 1654 A, 1052 C; 1238 G; 1919 T; 0 other;

XX XX

Query Match 4.7%; Score 155.2; DB 15; Length 5873;

Best Local Similarity 69.4%; Pred. No. 4e-31;

Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps

QY 693 GGTAAATGGATGCATGTCATATTTGGAGAAAGTCGACATGGTTTTATCTAATTCATGG 752

DB |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

DB 1176 GGTAAATGGCTGCTTATCGTACIATGATAAAGTTCTGATGGGTTTTATATGATCAATCG 1235

QY 753 GATGGACCCATAUGTATGGTGCATATGACCAATCTGGCAAGAGCATGGCGGATACCATC 812

DB |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

DB 1236 TCIGGATCCCTATATTTGGACCTTATGCATCGACCTGCATGAAAGTGGTGGCATCCCTTC 1295

QY 813 ATTTGAATCTCTGAAACAGTTGATTCAGCATCGGTTCATCAATGAAGTAGTTTGAT 872

DB |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

DB 1296 AATTGAATCAATTAAGAGCTGTGATTTCTGGTGTTGATTTCTGGCTTGAAGCGATCATAGT 1355

QY 873 AGATCGGCATAGTGCATGCTAGCTTAAAGAACTGCAAAACAGGCTGCATAATATTTCTC 932

DB |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

DB 1356 TGATAGGCGTAGTGCATCCAGCCTTCAAGGAACCTCACAAATAGAGTCCACGACATATCTG 1415

QY 933 CAGTTCTCTTAACCAACAAAAGAGGTTGCAGATCATATAGCAAAAGCTGGTATGCAATCACTT 992

DB |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

DB 1416 TAGCTGCAATTACCAACAAAAGAGGTTGTTGATCAGCTGGCAAAAGCTTATCTGCATCCGTAT 1475

QY 993 GGGG 996

DB ||||

DB 1476 GGGG 1479

RESULT 8

AAQ57912

ID AAQ57912 standard; DNA; 5890 BP.

XX XX

QY 693 GGTAAAGGATGATGATATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 752
DB 1598 GGTAAAGGATGATGATATATTTGGAGAAAGAGGAGAGATGGTTTATTAATGATGATGG 1657
QY 753 GATGAGAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 812
DB 1658 GGTAAAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 1717
QY 813 ATTTGAAATTTCTGAAAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAAT 872
DB 1718 AATTGAAATTTCTGAAAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAAT 1777
QY 873 AGATGAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 932
DB 1778 TGAATGAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 1837
QY 933 CAGTTGATGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 992
DB 1848 TAGTGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 1897
QY 993 GAGG 996
DB 1898 GAGG 1901

RESULT 12
AAT67128
ID AAT67128 standard; DNA: 6295 BP.
XX
AC AAT67128;
XX
BT 17-JUL-1997 (first entry)
XX
DE Constitutive triple response ctrl 2 mutation genomic DNA.
XX
KW CTR; Arabidopsis thaliana; mutant; agricultural; ethylene; ss.
XX
OS Arabidopsis thaliana.
XX
PN DS5602322 A.
XX
PO 11-FEB-1997.
XX
PE 10-AUG-1992; 92US-0928464.
XX
PR 17-JUN-1994; 94US-0261432.
PR 10-AUG-1992; 92US-0928464.
PR 12 JAN 1993; 93US 0003311.
XX
PA (GYPE) UNIV PENNSYLVANIA.
XX
PE Ecker JR, Kieber JJ;
XX
WP 1997:131867/12.

Plants over expressing constitutive triple response gene - resulting
in insensitivity to ethylene which can improve the quality and
longevity of crops e.g. by affecting fruit ripening
Claim 3: Column 37-44; 41pp; English.
The present sequence represents the ctrl 1-2 mutation of the constitutive
triple response (CTR) gene. The mutation is a 17bp deletion beginning at
position 1995 of the wild type genomic DNA which is predicted to result
in a frame shift in the coding region, and was produced by X rays. This
sequence is used to transform plant cells. The plants overexpress the
Arabidopsis thaliana CTR1 gene, which results in insensitivity to
ethylene. This benefits plants in relation to stress such as infection
due to pathogens (i.e. bacteria, viruses and fungi), wound healing and
soil penetration. Since ethylene affects agriculturally important
plant processes, e.g. fruit ripening, flower and leaf senescence and
leaf abscission, the ability to control ethylene sensitivity could

CC Improve the quality and longevity of crops.
XX
SQ Sequence 6295 BP; 1815 A; 1104 C; 1296 G; 2084 T; 606 A; 300 G;
Query Match 4.7%; Score 100.00; E-Value 1.0e-05; 100.00; 100.00;
Post-Scal Similarity 69.4%; Pred No. 3.00; Size 6295;
Matches 211; Conservation 99.99; Mismatches 99.99; 100.00; 100.00;
QY 693 GGTAAAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 752
DB 1598 GGTAAAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 1657
QY 753 GATGAGAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 812
DB 1658 GGTAAAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 1717
QY 813 ATTTGAAATTTCTGAAAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAAT 872
DB 1718 AATTGAAATTTCTGAAAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAAT 1777
QY 873 AGATGAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 932
DB 1778 TGAATGAGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 1837
QY 933 CAGTTGATGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 992
DB 1848 TAGTGGATGATGATATTTGGAGAAAGAGGAGAGATGGTTTATTAATTAATGATGG 1897
QY 993 GAGG 996
DB 1898 GAGG 1901
RESULT 13
AAQ98817
ID AAQ98817 standard; DNA: 6312 BP.
XX
AC AAQ98817;
XX
BT 19-JAN-1996 (first entry)
XX
DE Arabidopsis CTR1 genomic DNA.
XX
KW CTR1; constitutive triple response; transgenic; plant; ethylene;
KW stress tolerance; crop improvement; ss.
XX
OS Arabidopsis thaliana ecotype Columbia.
XX
PN DS5444166 A.
XX
PO 22 MAR 1995.
XX
PE 10 APR 1992; 92US-0928464.
XX
PR 12-JAN-1993; 93US 0003311.
PR 10-AUG-1992; 92US-0928464.
XX
PA (GYPE) UNIV PENNSYLVANIA.
XX
PE Ecker JR, Kieber JJ;
XX
WP 1995:302162/39.
XX
DE New constitutive triple response gene and mutant - constitutive
PT Arabidopsis thaliana, used to produce transgenic plants with
PT improved properties
XX
PS Claim 9: Column 31-38; 41pp; English.
XX
OS The CTR1 gene was mapped to an ethylene pathway. Ethylene
XX chromosome 5 of A. thaliana and a cDNA clone with the same
XX initiated using a YAC library. A sequence for the CTR1 gene was
XX obtained. Expression of the CTR1 gene in transgenic plants resulted in

CC dominant ethylene insensitive phenotype.
XX
SQ Sequence 6312 BP; 1818 A; 1107 C; 1297 G; 2090 T; 0 other;
Query Match 4.7%; Score 155.2; DB 16; Length 6312;
Best Local Similarity 69.4%; Pred. No. 4.2e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 693 GCTAAATGGATGCGATGTCATATTTGGAGAAAAGTGGAGATGGTTTTTATCTAATTCATCG 752
DB 1598 GGTAAAGGCTGCTATGCTACTATGATAAAGTTCTGATGGCTTTTATATATGATGATCG 1657
QY 753 GATGACCCCATATGTAAGGTCATTAATGACCAATTCGCAAGAGGATGGGCTATATCCAT 812
DB 1658 TGTGATGCTCATATTTGACCTTATGATCGAGCTGCATGAAAGTGTTCCTATGCTTT 1717
QY 813 ATTTAAATCTCTGAAAACAGATTGATTCGATGCTTCAATGAAATGAAATGAAAT 872
DB 1718 AATGAAATCATTAAGAGCTGTTGATTTCTGCTTGAATTTCTGCTTGAAGCTCATCAT 1777
QY 873 AGATGGCATAGTCTAGCTAGCTTAAAGAAAGTGCAGAAACAGGGTGCATATATTTCTTC 932
DB 1778 TGATAGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1837
QY 933 CAGTTCTGTAAACAGAAAGAGGTGTCATATGATGATGATGATGATGATGATGATGAT 992
DB 1838 TAGCTGCAITACACACAAAAGAGGTGTTGATGATGATGATGATGATGATGATGATGAT 1897
QY 993 GGGG 996
DB 1898 GGGG 1901
RESULT 14
AAQ98819 standard; DNA; 6312 BP.
XX
AC AAQ98819;
XX
DT 19-JAN-1996 (first entry)
XX
DE Arabidopsis CTRL-3 mutant genomic DNA.
XX
KW CTRL; constitutive triple response; transgenic plant; ethylene;
KW stress tolerance; crop improvement; mutagenesis; ss.
XX
OS Arabidopsis thaliana ecotype Columbia.
XX
PN US5444166-A.
XX
PD 22-AUG-1995.
XX
PF 10 AUG-1992; 92US-0928464.
XX
PR 12-JAN-1993; 93US-0003311.
PR 10-AUG-1992; 92US-0928464.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Ecker JR, Kieber JJ;
XX
DR WPI; 1995-302162/39.
XX
PT New constitutive triple response genes and mutants - isolated from
PT Arabidopsis thaliana, used to produce transgenic plants with
PT improved properties
XX
PS Claim 4; Column 43 50; 41pp; English.
XX
CC Seeds of A. thaliana ecotype Columbia were subjected to
CC ethylmethane sulfonate mutagenesis and screened for mutants that
CC constitutively displayed the triple response by plating on agar in the
CC absence of added ethylene in the dark. Sequence analysis of isolated

CC mutant ctrl-3 genomic DNA (given in AAQ98819) indicated a C to T
CC point mutation resulting in a stop codon at position 2701. 2703 of
CC the wild type genomic sequence (AAQ98817). Transgenic plants
CC expressing recessive ctrl mutations resemble ethylene-treated
CC wild type plants.
XX
SQ Sequence 6312 BP; 1818 A; 1106 C; 1297 G; 2091 T; 0 other;
Query Match 4.7%; Score 155.2; DB 16; Length 6312;
Best Local Similarity 69.4%; Pred. No. 4.2e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 693 GCTAAATGGATGCGATGTCATATTTGGAGAAAAGTGGAGATGGTTTTTATCTAATTCATCG 752
DB 1598 GGTAAAGGCTGCTATGCTACTATGATAAAGTTCTGATGGCTTTTATATATGATGATCG 1657
QY 753 GATGACCCCATATGTAAGGTCATTAATGACCAATTCGCAAGAGGATGGGCTATATCCAT 812
DB 1658 TGTGATGCTCATATTTGACCTTATGATCGAGCTGCATGAAAGTGTTCCTATGCTTT 1717
QY 813 ATTTGAATCTCTGAAAACAGATTGATTCGATGCTTCAATGAAATGAAATGAAATG 872
DB 1718 AATGAAATCATTAAGAGCTGTTGATTTCTGCTTGAATTTCTGCTTGAAGCTCATCAT 1777
QY 873 AGATGGCATAGTCTAGCTAGCTTAAAGAAAGTGCAGAAACAGGGTGCATATATTTCTTC 932
DB 1778 TGATAGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1837
QY 933 CAGTTCTGTAAACAGAAAGAGGTGTCATATGATGATGATGATGATGATGATGATGAT 992
DB 1838 TAGCTGCAITACACACAAAAGAGGTGTTGATGATGATGATGATGATGATGATGATGAT 1897
QY 993 GGGG 996
DB 1898 GGGG 1901
RESULT 15
AAQ98820 standard; DNA; 6312 BP.
XX
AC AAQ98820;
XX
DT 19-JAN-1996 (first entry)
XX
DE Arabidopsis CTRL-1 mutant genomic DNA.
XX
KW CTRL; constitutive triple response; transgenic plant; ethylene;
KW stress tolerance; crop improvement; mutagenesis; ss.
XX
OS Arabidopsis thaliana ecotype Columbia.
XX
PN US5444166-A.
XX
PD 22-AUG-1995.
XX
PF 10-AUG-1992; 92US-0928464.
XX
PR 12-JAN-1993; 93US-0003311.
PR 10-AUG-1992; 92US-0928464.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Ecker JR, Kieber JJ;
XX
DR WPI; 1995-302162/39.
XX
PT New constitutive triple response genes and mutants - isolated from
PT Arabidopsis thaliana, used to produce transgenic plants with
PT improved properties
XX
PS Claim 2, Column 51 58; 41pp; English.
XX

Query: "Vector: plasmidscript SK-; Site: 1; Ecoli; Site: 2; XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 48 days post inoculation with glomus versiforme. The cDNA was directionally ligated into the UniZap XR vector from Stratagene and packaged using GigaPack 111 Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex assist helper phage and propagated in XL10R cells."

BASE COUNT 149 a 136 c 177 g 221 t

ORIGIN

Query Match 12.1%; Score 493.2; DB 10; Length 684;
Best Local Similarity 74.7%; Prod. No. 66;
Matches 612; Conservative 3; Mismatches 170; Indels 4; Gaps 11

QY	557	GGAGAGAGGCTTGGCTTTTAAAGTTTCTTCAATONNACCTGGGGAGATGAGAGCAACT	616
DB	1	GGAGAGAGGCTTGGCTTTTAAAGTTTCTTCAATONNACCTGGGGAGATGAGAGCAACT	60
QY	617	TTATGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	676
DB	1	TTATGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	117
QY	677	TTATGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	746
DB	118	TTATGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	177
QY	747	TTATGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	796
DB	178	TTATGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	247
QY	797	ATGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	856
DB	238	ATGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	297
QY	857	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	916
DB	298	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	357
QY	917	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	976
DB	358	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	417
QY	977	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	1036
DB	418	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	477
QY	1037	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	1096
DB	478	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	537
QY	1097	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	1156
DB	538	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	597
QY	1157	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	1216
DB	598	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	657
QY	1217	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	1241
DB	658	TTGAGAGGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	692

RESULT 2
AW692841
LOCUS
DEFINITION
Accession
Version
Keywords

Source: barron medic
ORGANISM: Medicago truncatula
Eukaryotic; Viridiplantae; Streptophyta; Embryophyta; Eudicotyledons; Spermatophyta; Magnoliopsida; eucommidiales; Fabales; Fabaceae; Rosidae; eucosids 1; Fabales; Fabaceae; Euphorbiales; Euphorbiaceae; Medicago
REFERENCE: 1 (bases 1 to 659)
AUTHOR: Be/X. Zou, Shadler, G. J., Devitt, A. J., Barron, A. J., Devitt, A. J., Flores, H. R., Imman, J. L., Webster, C. W., May, J. L., and Devitt, A. J.
TITLE: Expressed Sequence Tags from the Medicago truncatula stem library
JOURNAL: Medicago truncatula stem library
COMMENT: Unpublished (2000)
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401-1074
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert length: 659 Std Error: 0.000
Plates: 056 Row: C Column: 06
Seq primer: TCACACAGGAAAACATATAGAT
FEATURES
location/Qualifiers
1..659
/organism "Medicago truncatula"
/db_xref "taxon:6080"
/clone "NF06650851"
/clone_lib "barron medic stem"
/tissue_type "stem"
/seq_stage "isolated direct clone"
/note "Vector: Lambda Zap phage; Helper: Ex assist"
internal stem segment

BASE COUNT 180 a 138 c 196 g 181 t

Query Match 11.9%; Score 493.2; DB 9; Length 684;
Best Local Similarity 76.8%; Prod. No. 66;
Matches 504; Conservative 3; Mismatches 149; Indels 4; Gaps 11

QY	1974	TTAAAGAGCTTGGAGAGAGGCTTCAATONNACCTGGGGAGATGAGAGCAACT	2574
DB	1	TTAAAGAGCTTGGAGAGAGGCTTCAATONNACCTGGGGAGATGAGAGCAACT	2564
QY	2039	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2099
DB	1	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2089
QY	2099	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2158
DB	122	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2148
QY	2158	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2217
DB	183	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2207
QY	2217	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2276
DB	243	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2266
QY	2276	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2335
DB	303	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2325
QY	2335	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2394
DB	363	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2384
QY	2394	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2453
DB	423	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2443
QY	2453	TTGATGCGATTCAGACGAGGACGCTTTTAAAGTGTATGATTTTCAAGTCAGAGCA	2512

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Db 483 CAGGAGTAATTTGAATGACGACAGAGTGTCTGCTGCGGTGGCTCAAGCATATAAAAGG 542
QY 2515 GTTGACATGCCACGTGATGTAATAATCCAAATTCGTTCTTAATAGTGGCTTGTCTGGGCG 2574
Db 543 GTGAGATGCAAGCAATTGAATCCACAAATAGCTGCAATAAATGAGAGCTTCTGCTGGGCG 602
QY 2575 GATGAGCCATGCAAAAGCGTCTCTCTTTTCCAGCATTTATGCAAAAGCTTGAACCAAT 2630
Db 603 AATGAGCCCTGCAAAAGCTCTCTTTTCCAGCATTTATGCAAAAGCTTGAACCAAT 2630
QY 2575 GATGAGCCATGCAAAAGCGTCTCTCTTTTCCAGCATTTATGCAAAAGCTTGAACCAAT 2630
Db 603 AATGAGCCCTGCAAAAGCTCTCTTTTCCAGCATTTATGCAAAAGCTTGAACCAAT 2630

RESULT 4
BE187627
LOCUS BE187627 652 bp mRNA linear EST 22 JUN 2000
DEFINITION Medicago truncatula cDNA clone pkv0-16119, mRNA
sequence.
ACCESSION BE187627
VERSION BE187627.1 GI:8666811
KEYWORDS EST.
SOURCE Medicago truncatula
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosidae; eucosids 1; Fabales; Fabaceae; Papilionoidae; Trifolium;
Medicago.
1 (bases 1 to 652)
VandenBosch, K., Endre, G., Hut, J., Moore, J., Beremand, P., Ellis, L.,
Town, C.D., Bowman, C.L., Graves, M.B., Hansen, T.S., Holt, J.E. and
Fraser, C.M.
ESTs from uninoculated seedling roots of Medicago truncatula
Unpublished (1999)
Contact: VandenBosch K
Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
Email: katemail.bio.tamu.edu
Texas A&M University name: T260803e
TIGR sequence name: MTGAU58TK
More information is available at:
http://bigzoo.cba.tamu.edu/medi-trp/
Seq primer: SKmod (CTA qAA CTA gta qAT CC).
Location/qualifiers
1..652
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/cultivar="genotype A17"
/db_xref="taxon:3880"
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/zellone lib="KV0"
/zissue_type="Seedling roots"
/zdes_state="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
/lab_host="E.coli strain XL0LR"
/vector="Vector: pBluescript SK+, Site1, PseF1, Site2.
XhoI: cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the UniLap XS vector from
Stratagene and packaged using GigaPack III Gold packaging
extracts. plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0LR cells."
BASE COUNT 180 a 125 c 158 g 189 t
ORIGIN

Query Match 11.6%, Score 331, DB 9, Length 652;
Best local Similarity 76.08; Pred. No. 1,1e-62;
Matches 484; Conservative 0; Mismatches 150; Indels 3; Gaps 1;

QY 1826 TTCCCTTGCTTAGAAATTTGGTTATTCATGGAACATCTTGATTTGACGACAAAA 1879
Db 16 TTCCCTTCCACATGGAGGATTTGGCCATACCATGGAGTGTCTTGTGTTTAAAGAAAAA 75
```

```

QY 1880 TTGAGACAGAGTTCCTTTTGGCACTGTAATACGTTGGTGGAGTGGTAAGGCTGAGATGTTGGT 1939
Db 76 TAGGATCAGAGTTCCTTTTGGCACTGTACATCTGTCGAGTGAATGCTTGGATGTTGGTGG 1939
QY 1940 TGAAGATGCTTCACAGAACACAGATTTGCAATGCTGAAAGTGTGTAATGAGATTTGAGAGAG 1999
Db 136 TTAATAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 195
QY 2000 TTGCTATCATGAAATCTTTTACGACATGCTTATATTTGATGCTTATGATGCTTATGATGCT 2059
Db 196 TTGCAATAATGAAACATTTTGGGCACTGCAAAACATTTGTTTATTAATGAGGAGATGATGAT 2059
QY 2060 AGGCAATCAAAATTTTGTGATGCTGCAAAACATTTGATGAGGAGATGATGATGATGATGAT 2119
Db 256 AAGCTCTAATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2119
QY 2120 TGCATAGTGTAGGTGTGCA--AAGACATAGATGAAACATGTAATGAAATGAAATGAAATGAA 2179
Db 316 TGCATAGATGAAATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 316
QY 2177 ATGCGGCAAGGGAATGAACTAGCTGCAAAACATTTGATGAGGAGATGATGATGATGATGAT 2236
Db 376 ATGCGGCAAGGGAATGAACTAGCTGCAAAACATTTGATGAGGAGATGATGATGATGATGAT 436
QY 436 TAAATGCAAAATTTGATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 495
Db 436 TAAATGCAAAATTTGATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 495
QY 2297 TCTGCGCTTAAAGGCAAGGGAATGAACTAGCTGCAAAACATTTGATGAGGAGATGATGATGAT 2356
Db 496 TCTGCGCTTAAAGGCAAGGGAATGAACTAGCTGCAAAACATTTGATGAGGAGATGATGATGAT 555
QY 2357 GATGCGCAGCAGCAATGAACTAGCTGCAAAACATTTGATGAGGAGATGATGATGATGATGAT 2416
Db 556 GATGCGCAGCAGCAATGAACTAGCTGCAAAACATTTGATGAGGAGATGATGATGATGATGAT 615
QY 2417 TTGCAAGTCAATTTTGTGGGAGTGGCAACATTTTGTCAACA 2453
Db 616 TTGCGGTAATTCATGTTGGGAGATTTGCAACATTTGTCAACA 652

RESULT 4
BE555627
LOCUS BE555627 581 bp mRNA linear EST 04 MAR 2001
DEFINITION Gm-c1045-2205 5' similar to SW:GRI_ARAH_Q05609;
SEEINE/THFECNINE PROTEIN KINASE GRI1, GRI2, GRI3 sequences.
ACCESSION BE555627
VERSION BE555627.1 GI:9820117
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosidae; eucosids 1; Fabales; Fabaceae; Papilionoidae; Phaseolaceae;
Glycine.
1 (bases 1 to 581)
Shenolik, E., Fels, P., Vukobratovic, E., Hladikova, J., Vukobratovic,
A., Bolla, B., Marra, M., Hillier, L., Kucuk, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Chelishchuk, B., Allen, M., Lawless,
Y., Person, B., Swaller, T., Gibbons, M., Raper, P., Harvey, N., Schork,
R., Ritter, E., Kohn, S., Shin, J., Jackson, Y., Cardenas, M., Morgan,
R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shenolik E/Fablab Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63106, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2140
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QY 1271 GGGCAGGTTGCTTAAGCCAAAGGAGATTCTTTGGTCAAAATGGTCCATCATCCCAATTC 1330
Db 422 ATCCAGAGATGTTATCTGAACCAAAATTCATGCTCAATGGTCCATCTTCCATCTCGATT 481

QY 1331 CTTGACCAATTCGATTTCCAGAGACAAAACCTATATGAATCTACCAATTCGATTCAGGTCAC 1390
Db 482 CTTGACCAATTCGATTTCCAGAGATTCGACAAAGTTGAACCTGCCAUGGATTCACGTCAC 541

QY 1391 TGGCAACACAGTATTTCTTGGATGAGCAATCACTTAATCTTGTATTGTATGA 1442
Db 542 TGGCAACACAGTATTTCTTGGATGAGCAATCACTTAATCTTGTATTGTATGA 593

RESULT 6
LOCUS BM410008 798 bp mRNA linear EST 22-JAN-2002
DEFINITION EST584345 tomato breaker fruit Lycopersicon esculentum cDNA clone
ACCESSION BM410008
VERSION BM410008.1 GI:18261638
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 798)
AUTHORS Alcalá, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai,
J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S., Ronning,
C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D., and Giovannoni, J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished (2002)
CONTACT: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genomics.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
FEATURES
Location/Qualifiers
1..798
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG51G17"
/clone_lib="tomato breaker fruit"
/tissue_type="pericarp"
/dev_stage="breaker"
/lab_host="SOL"
/note="Vector: pBluescriptSKmCuadapt; Site_1: EcoRI;
Site_2: XhoI; supplier: Boyce Thompson Institute;
Sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
BASE COUNT 227 a 138 c 198 g 235 t
ORIGIN

Query Match 10.7%; Score 353; DB 10; Length 798;
Best local similarity 76.2%; Pred. No. 2,3e-57;
Matches 461; Conservative 0; Mismatches 140; Indels 4; Gaps 2;

QY 1819 CTTGACCTGGCTTACAGAGATTGGTTATTCGATCGACAGATCTTGATTGAGGAGAAA 1878
Db 180 CTGTGCTTGATGATGAGAGATCTGGATATTCGCTGGCAATGATCTGCTTCTCAGCAACA 239

QY 1879 ATTGGACAGGCTCTTTTGGGACGATATCGCTGGTGGTGGAGTGGCATGGCTCGATCTGCT 1928
Db 240 ATTGGGACAGGCTCTTTTGGGACGCTGTCGACTGCGACTGGAATGGCTTCGATCTGCT 299

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QY 1939 CTCACAGATGCTGTACACACAAACAGACCTTCTTAATGAGAGAGAGAGAGAGAGAG 1998
Db 300 GTGAAAATTCATCATGGAACAGGATTTTCTATGTTGAGCGATAAAGGAAATTTTAAAG 359

QY 1999 GTTCTCATCATCAAAATCTTTACGACATCTTAAATATCTACATGTTTATGAGAGAG 2058
Db 360 GTTGCAATATCAAGCGGTTCCGACATCGCAAAATATAGTCTTTTATGAGGAGGTTTAA 419

QY 2059 AAGCCACCAAACTTTGTCATTGTCAGAGAAATATCTATGAGAGAGAGAGAGAGAG 2118
Db 420 GAGCCACCAAACTTTGTCATTGTCAGAGAAATATCTATGAGAGAGAGAGAGAGAG 479

QY 2119 TTGCATTAAGTCACCTGTCTCAAAACATA CAAGAAACATTTGAAATAGAAATTTT 2178
Db 480 CTTCATAAACCTGGTGGAGAGAGAGATTCGATCAAAAACGTGGTTGTTGATATGATTA 539

QY 2176 CATGTGCAAAAAGGCAATGAACTACCTGCAATAGAGAGAGAGAGAGAGAGAGAGAG 2235
Db 540 CATGTGCAAAAAGGCAATGAACTACCTGCAATAGAGAGAGAGAGAGAGAGAGAGAG 599

QY 2236 TTAATAATACCGGAATCTGTGTAGTTGATCAAGAAATATAGAAATTTTAAATTTT 2295
Db 600 TTAATAATCTCCAAATCTTTTAGTGGATACAAAATATACAGTGAAGGTTGTTGATTTT 659

QY 2296 CTGTCCTCTTTAAAGCCACCGATAATCTTCTTCAATTAATCTGAAATTTGAAAT 2355
Db 660 CTCTCTCGATTAAA-GCTAATACATTTTCTGATCAATTAATCTGAAATTTGAAAT 719

QY 2356 TCGATCCCAACCAAGTACTACTAGCGATGAAACCAACAAATGAAAGATTTGATAG 2415
Db 719 TCGATCCCAAGTCTCAAAATCTTCTGATGAAACCAACAAATGAAAGATTTGATAG 778

QY 2416 TTTCG 2420
Db 779 TTTCG 783

RESULT 7
LOCUS BI422885 720 bp mRNA linear EST 19-APR-2000
DEFINITION EST533551 tomato callus, TAMU Lycopersicon esculentum cDNA clone
ACCESSION BI422885
VERSION BI422885.1 GI:15197663
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 720)
AUTHORS Alcalá, J., Vrebalov, J., White, R., Matern, A., Vision, T., Bougri,
O., Liang, F., Upton, J., Craven, M.B., Bowman, J., Allen, S., Ronning,
C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D., and Giovannoni, J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)
CONTACT: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genomics.clemson.edu/orders/index.html
Location/Qualifiers
1..720
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG71P14"
/clone_lib="tomato callus, TAMU"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-blue MRP"
FEATURES
Source

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QY 2221 ATTGTTTCATGCTGATTTTAAATTCAGTGAATCTGTTAGTTGACAGANGANGATATACAGTCAAG 2280
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DB 257 ATTGTTTCATGCTGATGCTGAGTCACTAATCTTTTGTGTTGATAAGAAGTGGAAATGTTAAG 316

QY 2281 GTTGTGAGATTTTGGTCTCTCCGTTTAAAGGCGACGACATTTCTTTTCATCCAAATCTGCA 2340
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 317 GTAGGTGATTTTGGCTTGTCTGCTGAGGACACAACTATTTTGTCTTCCAAATCAACA 376

QY 2341 CCTGCAACACCTGAATGGAATGGACACCAAGTACTAGCGGATGAACCATCAAAATGAAAAG 2400
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 377 GCTGGAACGCTGATGCGATGGAGGCAACAGAAATTTCTGCAATGAACTTTGAAATGAGAAG 436

QY 2401 TCAGATGTTTACAGCTTTTGGAAATGATTTTCTGGAAATTTGCAAACTTTGCAACAGCCATGG 2460
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DB 437 TGTGACATCTACAGTTTGTGCTGCTATCTATGCGAACTTGTACCTTAAGATTAAGCTTTGG 496

QY 2461 TGTAAAGTAAAGCCATCAAGCTTCTGCTGCAAGCTCTGCAATTTAAAGGCAAAAGGCTTGAC 2520
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DB 497 AGTGAATGAATCTATGCAAGTGGTGGAGCTGTTGGCTTCCAGAAATAAAGCGCTTGAA 556

QY 2521 ATCCACCTGCAATTAATAATGCAAAATTTGCTTAAATGCTGCTGCTGCTGCTGCTGCTGCTG 2580
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DB 557 ATCCCAAGGAATCTATGCTATAGTAGCAAGAAATATATGCGAAATGTTGCAAACTGAT 616

QY 2581 CCATGCAAAAGTCTCTCTTTTCCAGCAITATGCAAAAGCTTCAAAAGC 2627
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DB 617 CCAAACTTGGTGGCAATTTGCCACAGCTAACTGTGGCTTTAACACC 663

RESULT 15
RG129283 759 bp mRNA linear EST 31-JAN-2001
LOCUS EST4747929 tomato shoot/meristem Lycopersicon esculentum cDNA clone
DEFINITION cTOF2334 5' sequence, mRNA sequence.
ACCESSION RG129283
VERSION RG129283.1 GI:12629471
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryote, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 759)
AUTHORS van der Hoeven,R., Pezzarides,D., Sun,H., Cho,J., Utterback,F.,
Hansen,C., Renning,C. and Tanksley,S.
TITLE Generation of ESTs from tomato shoot/meristem tissue
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genomics.clemson.edu/gen/index.html.
FEATURES
Source
Location/Qualifiers
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/cultivar="LA496"
/db_xref="taxon:4081"
/clone="cTOF2334"
/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/notes="Vector: pBluescript SK(-), Site_1: EcoRI, Site_2:
XhoI; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."
BASE COUNT 209 a 127 c 228 g 215 t
ORIGIN
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Query Match 8.0%, Score 264.2; DB 10; Length 759;
Best Local Similarity 64.6%; Pred. No. 1.9e-40;
Matches 427; Conservative 0; Mismatches 228; Indels 6; Gaps 2;

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QY 1897 AAAAAAATCAAGCTTCCGCTGGCTTGAAGAGATTTGGTTATTTCAAGGAGAGATTTGGAT 1900
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DB 55 AAATCTGATGACACTTGATGATGTCGAGATTTGTCAGATTTCAAAAGGAGAGATTAAT 114

QY 1867 TTGAGGAGAGAAAATTTGAGCAGAGCTTCTTTGGGAGCTGATATTTGGTGGATGGT 1926
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DB 115 TTGGGTGAGGCTATGCGACTTGGATCTTATGCGAGGCTATTTGAGAGAGTGGTATGGA 174

QY 1927 TCTGATGTTGCTGTGAAGATCCTCACAGAACAAAGACTTCCATCCTGAACGTGTTAAAG 1986
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 175 ACTGAAGTAGCTGTGAAGAAAATTTCTAGACCAAGAAATTAACCTGGTGAATTAATTTGA 244

QY 1987 TTTCTGAGAGAGGTTGCTATCATGAATCTTTACGACATCTTAATATGTTTAAAG 2046
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DB 235 TTIAAAAGTGAAGGTGATGATCATGAAAAGACTCCGCACTCCCTAAAGTCTGTTCAAT 294

QY 2047 CATTGGGTGAGAAAGCACTCAAAAGTGGTAAAGGATTAATATGCTATTTGAAAGGTAAT 2100
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DB 295 GGAGCTGTTACACGCTCTCCAAAGCTTTCAATTTGTTAGTAGAGTTTCTAATAGAGT 354

QY 2107 TCTATAGGCTTTTGGCATTAAGTCAAGGCTGTAAGGATTAATATGAGGATTAAT 2160
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DB 355 TTATACAGATTAATTCATCGGTC GAACAATCAATTATAGATGAACAGATTTGAGG 411

QY 2167 ATGGCTTTTATGTGGCAAAAGGGAATGAACCTGCAATACAGCTGATCTTCAATTTG 2220
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DB 412 ATGGCTCTTGATGCTGCTGGAGGAAATGAACATATACACAAATTTGATCTTTGATAG 471

QY 2227 CATGCTGATTTTAAATACCGGAATCTGTTAGTTCAAAAGAGATTAATTAAGGTTTGG 2280
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DB 472 CATGCTGATTTGAAGTCTCTTAATCTGTTTGGGATAAGAAATGGCTTGTAAAGGTTAT 531

QY 2287 GATTTTGGTCTCTGCTGTTTAAAGGCAAGGAAATTTCTGATTAATTAATTAATTA 2340
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DB 532 GATTTTGGGTTATGCAAAATTAAGGCAAGGAAATTTCTGATTAATTAATTAATTAAT 591

QY 2347 ACAGCTGAATPGGATGGCAGACAGAAATAGTACAGGCAATTAATTAATTAATTAAT 2400
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DB 592 ACCGCTGAGTGGCATGCTGCTGCAAGGCTTCAAGATCAAGGCTTCAAGATCAAGGCT 651

QY 2407 GTTACACAGCTTTTGGAGTGAATTTCTCT--CGGAGTTGGCAATTTGCAATTAATTA 2460
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DB 652 GTATATAGCTTTTGGGTTGTGATCTATGAGGAGGCTTTGTTATTTGTAATTAATTA 711

QY 2464 A 2464
DB 712 A 712
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Search completed: October 22, 2002, 10:40:37
Job time : 2482 secs

denCore version 5.1.3
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OM nucleotide - nucleotide search, using sw model
Run on: October 22, 2002, 08:46:10, Search time 71 seconds
(without alignments)
11368.334 Million cell updates/sec

Title: US-09-904-389-1
Perfect score: 3286
Sequence: 1 attcatttctcgaagagaa.....aaaaaaaaaaaaaaaaaaaa 3286

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB Seq length: 0
Maximum DB Seq length: 2000000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued patents, NA: *
1: comp2_511_1111_1111_5A_OMP.seq.*
2: comp2_511_1111_1111_5B_OMB.seq.*
3: comp2_511_1111_1111_5A_OMB.seq.*
4: comp2_511_1111_1111_5B_OMB.seq.*
5: comp2_511_1111_1111_5A_OMB.seq.*
6: comp2_511_1111_1111_5B_OMB.seq.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	898.8	27.4	2890	1	US-07-928-464-1 Sequence 1, Appli
2	898.6	27.4	2890	5	PCT-US93-07347-1 Sequence 1, Appli
3	898.8	27.4	3033	1	US-08-003-311B-1 Sequence 1, Appli
4	898.8	27.4	3033	1	US-08-261-432-1 Sequence 1, Appli
5	155.2	4.7	5875	1	US-07-928-464-4 Sequence 4, Appli
6	155.2	4.7	5875	5	PCT-US93-07347-4 Sequence 4, Appli
7	155.2	4.7	5890	1	US-07-928-464-3 Sequence 3, Appli
8	155.2	4.7	5890	1	US-07-928-464-5 Sequence 5, Appli
9	155.2	4.7	5890	1	US-07-928-464-6 Sequence 6, Appli
10	155.2	4.7	5890	5	PCT-US93-07347-3 Sequence 3, Appli
11	155.2	4.7	5890	5	PCT-US93-07347-5 Sequence 5, Appli
12	155.2	4.7	5890	5	PCT-US93-07347-6 Sequence 6, Appli
13	155.2	4.7	6295	1	US-08-003-311B-4 Sequence 4, Appli
14	155.2	4.7	6295	1	US-08-261-432-4 Sequence 4, Appli
15	155.2	4.7	6312	1	US-08-003-311B-3 Sequence 3, Appli
16	155.2	4.7	6312	1	US-08-003-311B-5 Sequence 5, Appli
17	155.2	4.7	6312	1	US-08-003-311B-6 Sequence 6, Appli
18	155.2	4.7	6312	1	US-08-003-311B-7 Sequence 7, Appli
19	155.2	4.7	6312	1	US-08-261-432-3 Sequence 3, Appli
20	155.2	4.7	6312	1	US-08-261-432-5 Sequence 5, Appli
21	155.2	4.7	6312	1	US-08-261-432-6 Sequence 6, Appli
22	155.2	4.7	6312	1	US-08-261-432-7 Sequence 7, Appli
23	81.6	2.5	1365	3	US-09-221-237-6 Sequence 6, Appli
24	81.6	2.5	1365	3	US-09-221-237-6 Sequence 6, Appli
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28	81.6	2.5	1365	4	US-09-221-245-6 Sequence 6, Appli
29	81.6	2.5	1365	4	US-09-163-115-6 Sequence 6, Appli
30	81.6	2.5	1365	4	US-09-221-528-6 Sequence 6, Appli
31	81.6	2.5	1365	4	US-09-593-553-6 Sequence 6, Appli
32	81.6	2.5	1365	4	US-09-221-237-6 Sequence 6, Appli
33	81.6	2.5	2120	3	US-09-221-237-4 Sequence 4, Appli
34	81.6	2.5	2120	3	US-09-221-928-4 Sequence 4, Appli
35	81.6	2.5	2120	3	US-09-221-527-4 Sequence 4, Appli
36	81.6	2.5	2120	3	US-09-221-236-4 Sequence 4, Appli
37	81.6	2.5	2120	3	US-09-221-416-4 Sequence 4, Appli
38	81.6	2.5	2120	4	US-09-221-245-4 Sequence 4, Appli
39	81.6	2.5	2120	4	US-09-163-115-4 Sequence 4, Appli
40	81.6	2.5	2120	4	US-09-221-528-4 Sequence 4, Appli
41	81.6	2.5	2120	4	US-09-593-553-4 Sequence 4, Appli
42	81.6	2.5	2120	4	US-09-221-237-4 Sequence 4, Appli
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44	73.8	2.2	3681	1	US-08-909-984A-3 Sequence 3, Appli
45	73.8	2.2	3681	1	US-08-909-984B-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-07-928-464-1
; Sequence 1, Application US/07928464
; Patent No. 5367065
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENTS: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock, Washburn, East - My Viewers and
; ADDRESS: No. 5367065ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; ATTORNEY NAME: 07928,464
; FILING DATE: 19920810
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2890 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2583
US-07-928-464-1

Query Match: 27.4%; Score 898.8; DB ID: Length 2890;
Best local similarity: 64.3%, Pred. No. 6, 50-245;
Matches 1592; Conservative: 0; Mismatches: 664; Indels: 216; Gaps: 7;
US-07-928-464-1

Db 1297 AGGTTGGGCTTGATAGAGAGTAGGCTGGTGTGATTTACTAGCAAAAGGAGGCTCACTTATGG 1356
QY 1288 CAACCTGATCTTTGCTCAATGGTCCCATCAATCCATCTCAATTTCTTCCACCATTTGGGATTT 1347
Db 1357 GAGGCTGATCTCTTCTAAATGGTCTTCACTATCTCAATTTCTTCTCTCTCTGCGGTTT 1416
QY 1348 CCAAGACTAAACCTATTCGAATCTACCATTTGATTTTCAGGTCACATGGGCAAAACAGTATTTG 1407
Db 1417 CCAGGACCAAGGACATTCGAACCGGCGAGTCGATTTTAGGTTACTAGCCCAAAACAATATTC 1476
QY 1408 TTGATAGCCCAATCACTTAATCTTGTATTTTATGATGAAGCTTCTTCAGGTAATGTGTGATCT 1467
Db 1477 TCGGATAGCCAGAGCTTAATCTTGTTCGATCTCTGCATCAG----- 1519
QY 1468 GGGAGGATGCTGCAATTCGGGCTCTATCAAGGCCATTAATATAGGAAGGATGTAGATGGA 1527
Db 1520 ----ATGATAGGGATTCTCAATGTTTCTATAGGCAATATGATAATCCGCGTGGAGAGAAAT 1575
QY 1528 AAAACCATAGTGTGTACCTGCTGACAGGACAGAGAAATTCCTCAGTTATTAATAAAAAAGCA 1587
Db 1576 GAGGCATGGGAGAAAAATGGTG----- 1597
QY 1588 GCCCAACTGAATACTCAAGATGGAAGAGCTGAGCAATTTAGATCATGTGTGCTTCTCCA 1647
Db 1598 ----- 1597
QY 1648 TATAGTGATAGTGGAGCGGCTTTTGTAGAAAAATGTAGTCCCTTTAAGCCATATCTCACAC 1707
Db 1598 -----GTGGGCTCTTGGCCACCC 1614
QY 1708 ATGGGTCGGAAGATTCGGAGCATCTCTTAGCATCTGTCATCCCAAGGATGGATCATGTT 1767
Db 1615 AGTGCTAATATGCTCCACAGAACATGATCGTGCGGTCAAATCAATTTGAAGCAGCACCT 1674
QY 1768 AACAAATTTACCATTTGTTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 1827
Db 1675 ATGAATGCCCCCAATCAGTCAGCCAGTTCACAAACAGGCAATACGGAACCTTGGACTT 1734
QY 1828 GGCTTAGAAGATTTGGTTATTCATGACAGATCTTGTGATTTGAGGAGAGAAAAATTTGGAGCA 1887
Db 1735 GATGGTGATGATATGACATCCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1794
QY 1888 GGTCTCTTTGGGACCTGATATATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1947
Db 1795 GGTCTCTTTGGGACCTGATATATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1854
QY 1948 CTCACAGAACAGACTTCCTATCTGAAAGGCTGATGATGATGATGATGATGATGATGATGATG 2007
Db 1855 CTCATGAGACAGACTTCCTATCTGAAAGGCTGATGATGATGATGATGATGATGATGATGATG 1914
QY 2008 ATGAATCTTTAGACATCTCTAATATTTGATGATGATGATGATGATGATGATGATGATGATG 2067
Db 1915 ATGAAGGCTCTGCGACGCTTAACATTTGTCATGATGATGATGATGATGATGATGATGATGATG 1974
QY 2068 AACTGTGTCATGTCACCGAATAATATATGAGAGAGGATGATGATGATGATGATGATGATGATG 2127
Db 1975 AATTTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2034
QY 2128 TCAGGTGTCA---AAGACATAGATGAAGAACACAGTCCGAATAAATATGGCTTTTGTATGGCA 2184
Db 2035 AGTGGAGCAAGGAGCAATATAGATGAGAGAGGCTGGCTGATGATGATGATGATGATGATGATG 2094
QY 2185 AAGGGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2244
Db 2095 AAGGGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2154
QY 2245 CCGAATCTGTTAGTTCAGCAAGAGATATACAGTCAAGGTTTGTGATTTTGTGCTGCTGCGCT 2304
Db 2155 CCAAACTTATGTTGATGACAAAAAATATACATGCAAGTTTGTGATTTTGTGCTGCTGCGCT 2214
QY 2305 TTAAGGACGACGATTTTCTTATCCCAATTTGAGGCTGGGAACGCTGAATGATGATGATGATG 2364
Db 2215 TGAAGGACGACGCTTCTTTCTCGAAGTACAGGCTGGAAACCGGAGTGAATGATGATGATG 2374

QY 2365 CCAGAAAGTACTACGGGATGACCATCAAAATGAAAAGTCAGATGATGATGATGATGATGATGATG 2424
Db 2275 CCAGAAAGTACTACGGGATGACCATCAAAATGAAAAGTCAGATGATGATGATGATGATGATG 2334
QY 2425 ATTTGCTCCGACTTGGCAACTTGGCAACTTGGCAACTTGGCAACTTGGCAACTTGGCAACTTGG 2484
Db 2335 ATCTTGTGGGAGCTTGTCTACATTCACCAACCAACCAATGGGTAACCTTAAATGATGATG 2394
QY 2485 GTCCGAGCTGTGTGGATTTAAGGCAAAAGGCTTGACATGATGATGATGATGATGATGATGATG 2544
Db 2395 GTACCTCGGCTTGGTTTCAAGCTGTAAAGGCTGGAGATCGGCGGTAATGATGATGATGATG 2454
QY 2545 TTGGCTTCTTAAATAGTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 2604
Db 2455 GTTCAGGCAATATCGAGGCTTGTGAGCAATGAGGCAATGAGGCAATGAGGCAATGAGGCA 2514
QY 2605 AGCATATGGAAGGCTTGAAGCAATGACTAAACCAAGGCAATGCAAAAGGCAATGCAAAAGG 2664
Db 2515 ACTAATATGGACTTGTCTAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2574
QY 2665 GA 2666
Db 2575 GA 2576

RESULT 5
US-07-928-464-4
; Sequence 4, Application US/07928464
; Patent No. 5367065
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: No. 5367065ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07928,464
; FILING DATE: 19920810
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5873 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US 07 928 464 4

Query Match 4.73, Score 155.23, E-Value 1.0e-33
Best Local Similarity 69.48; Pred. No. 2.5e-32;
Matches 211, Conservative 6, Mismatches 33, Gaps 00

QY 693 CTTAAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 702

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Db 1176 GATTAAGGCTGTTATGCTACATGATAAAGTTCGTGATGGGTTTATATGATGAAATGG 1235
QY 753 GATGACCCATATGATGCTCATTAAGCACCAAATCTGCAAGAGGATGGGGATACCATC 812
Db 1236 TCTGATCCCTATATTTGGACCTTAGCATCGACCTGCATGAAAGTGGTGGCATCCCTTC 1295
QY 813 ATTGAAATCTCTGAAAACAGTTGATTCACGATCGGTTTCATCAATTCAGAGTAGTTTGGAT 872
Db 1296 AATTGAATATTAAAGAGCTGTGATTCCTGGTGTGATTCCTGCGTTGAAGGATCATAGT 1355
QY 873 AGATCGGCTATAGTATGCTAGCTAGCTTAAAGAACTGCAAAACAGGCTGCATATPATTTCTTC 932
Db 1356 TGATAGGCTAGTATGATCCAGCTTC'AAGGAACTTCACATAGAGTCCAGGACATATCTTG 1415
QY 933 CAGTTGTGTAAACCAAAAAGAGGTTGACATCATATAGCAAAAGCTGGTAIGCAATCATTT 992
Db 1416 TAGTGCATTAACCAAAAAGAGGTTGTGATCATCGCTGGCAAGCTTATCTGCAATCGTAT 1475
QY 993 GGGG 996
Db 1476 GGGG 1479
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RESULT 6

PCT US93-07347 4

Sequence 4: Application PC/TUS9307347

GENERAL INFORMATION:

APPLICANT: Ecker, Joseph R.
APPLICANT: Kiebel, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and

ADDRESSEE: Norris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PC/9307347

FILING DATE: 19930805

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Miller, Suzanne E.

REGISTRATION NUMBER: 32,279

REFERENCE/DOCKET NUMBER: JPN-1086

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215 568-3100

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 5873 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT US93-07347-4

Query Match

Best Local Similarity 69.48% Prod. NO: 2560-327

Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

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QY 693 GGAATGGATGATGATCATATTGGAGAAAAGTGGCAGATGGTTTTTAATCTAATTCATGG 752
Db 1176 GGTAAATGGCTGCTATGCTAGTATGATAAAGTTCGTGATGGGTTTATATGATGAAATGG 1235
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QY 753 GATTAAGGCTGTTATGCTACATGATAAAGTTCGTGATGGGTTTATATGATGAAATGG 1235
Db 1236 TCTGATCCCTATATTTGGACCTTAGCATCGACCTGCATGAAAGTGGTGGCATCCCTTC 1295
QY 813 ATTGAAATCTCTGAAAACAGTTGATTCACGATCGGTTTCATCAATTCAGAGTAGTTTGGAT 872
Db 1296 AATTGAATATTAAAGAGCTGTGATTCCTGGTGTGATTCCTGCGTTGAAGGATCATAGT 1355
QY 873 AGATCGGCTATAGTATGCTAGCTAGCTTAAAGAACTGCAAAACAGGCTGCATATPATTTCTTC 932
Db 1356 TGATAGGCTAGTATGATCCAGCTTC'AAGGAACTTCACATAGAGTCCAGGACATATCTTG 1415
QY 933 CAGTTGTGTAAACCAAAAAGAGGTTGACATCATATAGCAAAAGCTGGTAIGCAATCATTT 992
Db 1416 TAGTGCATTAACCAAAAAGAGGTTGTGATCATCGCTGGCAAGCTTATCTGCAATCGTAT 1475
QY 993 GGGG 996
Db 1476 GGGG 1479
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RESULT 7

PCT US93-07347 4

Sequence 4: Application US/0792849 4

Patent No. 5467065

GENERAL INFORMATION:

APPLICANT: Ecker, Joseph R.

APPLICANT: Kiebel, Joseph J.

TITLE OF INVENTION: Constitutive Triple Response Gene and

TITLE OF INVENTION: Mutations

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and

ADDRESSEE: Norris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/9307928,494

FILING DATE: 19920810

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Miller, Suzanne E.

REGISTRATION NUMBER: 32,279

REFERENCE/DOCKET NUMBER: JPN 1086

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215 568-3100

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 5890 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: Intron

LOCATION: 1..353

FEATURE:

NAME/KEY: Exon

LOCATION: 354..1061

FEATURE:

NAME/KEY: Intron

LOCATION: 1002..1176

FEATURE:

NAME/KEY: Exon

LOCATION: 1177..1477

MOLECULE TYPE: DNA (genomic)

Transcript: PTC1 - CMT1A (NM_000053.5)		
FEATURE:	NAME/KEY:	intron
	LOCATION:	1..353
FEATURE:	NAME/KEY:	exon
	LOCATION:	354..1001
FEATURE:	NAME/KEY:	intron
	LOCATION:	1002..1176
FEATURE:	NAME/KEY:	exon
	LOCATION:	1177..1477
FEATURE:	NAME/KEY:	intron
	LOCATION:	1478..1574
FEATURE:	NAME/KEY:	exon
	LOCATION:	1575..1719
FEATURE:	NAME/KEY:	intron
	LOCATION:	1720..1936
FEATURE:	NAME/KEY:	exon
	LOCATION:	1937..2038
FEATURE:	NAME/KEY:	intron
	LOCATION:	2039..2173
FEATURE:	NAME/KEY:	exon
	LOCATION:	2174..2379
FEATURE:	NAME/KEY:	intron
	LOCATION:	2380..2736
FEATURE:	NAME/KEY:	exon
	LOCATION:	2737..3012
FEATURE:	NAME/KEY:	intron
	LOCATION:	3013..3202
FEATURE:	NAME/KEY:	exon
	LOCATION:	3203..3243
FEATURE:	NAME/KEY:	intron
	LOCATION:	3244..3519
FEATURE:	NAME/KEY:	exon
	LOCATION:	3520..3588
FEATURE:	NAME/KEY:	intron
	LOCATION:	3589..3668
FEATURE:	NAME/KEY:	exon
	LOCATION:	3669..3769
FEATURE:	NAME/KEY:	intron
	LOCATION:	3770..3858
FEATURE:	NAME/KEY:	exon
	LOCATION:	3859..3943
FEATURE:	NAME/KEY:	intron
	LOCATION:	3944..4037
FEATURE:	NAME/KEY:	exon
	LOCATION:	4038..4136
FEATURE:	NAME/KEY:	intron
	LOCATION:	4137..4369
FEATURE:	NAME/KEY:	exon
	LOCATION:	4370..4438

?	FEATURE:		
?	NAME/KEY:	intron	
?	LOCATION:	4439..4541	
?	FEATURE:		
?	NAME/KEY:	exon	
?	LOCATION:	4542..4673	
?	FEATURE:		
?	NAME/KEY:	intron	
?	LOCATION:	4674..4787	
?	FEATURE:		
?	NAME/KEY:	exon	
?	LOCATION:	4788..4892	
?	FEATURE:		
?	NAME/KEY:	intron	
?	LOCATION:	4893..4959	
?	FEATURE:		
?	NAME/KEY:	exon	
?	LOCATION:	4960..5056	
?	FEATURE:		
?	NAME/KEY:	intron	
?	LOCATION:	5057..5890	
?	pct-us93-07347-3		

Query Match	4.7%	Score 155.2	EB 5	Length 589
Best Local Similarity	69.4%	Pred. No. 2.5p-32		
Matches 211: Conservative	0	Mismatches 93	Indels 0	Clips 0

QY	693	GCTAAATGGCATGTCATATTTCACAGAAAAGTGGACATAAGTTTTAATTAATTTATAAGT	762
DB	1176	GCTTAATCGGTGCTTATCGTACTACTATGATAAAGTTGTTCAATGGTTTTATAAGAGAAGATAG	1245
QY	753	GAAGGACCACATATGCTATGCTCATTATGCANNAATATCCAAAGAGATAGAGGTTATATATATAT	812
DB	1236	TCTGGATGCCATATATTGGACCTTATGCATCGACNTGGATCAAAGTGGTGCAATATTT	1295
QY	813	ATTCTAATCTCTGAAAAACACTTGATTCACAGCATCGGTTCATCAATATGAAGTAGTTTTGAT	872
DB	1296	AATTGAATCATTAAGAGCGTCTTCATCTCTGGTGTGATTTCTTGGTTGAAGAGGATATAAGT	1355
QY	873	ACATCGGCATAGTGTGATGCTTACCTTAAAGAACCTGCAAAAACAGGCTGGCATAAATATCTT	932
DB	1356	TGATAGCGGTAGTGATCCACGCTTTCAGGAACCTTCACACATAGAGTCAAGATATCTTGG	1415
QY	933	CAGTTGTGTACCCACAAGAGAGGTTCACAGATCAATAGCAAAAGTGGTATGTAATATATTT	992
DB	1416	TAGCTGCCATACCCACAAAAGAGGTGTTTCAICAGTTGGGCAAAAGCTTATCTGCAATATGTAAT	1475
QY	993	CTGGG	996
DB	1476	GGGG	1479

RESULT 11
PCT-US93-07347-5
; Sequence 5, Application PC/TUS9307347
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Woodcock, Washburn, Kurtz, Markiewicz and
; ADDRESSER: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/928,464
;; FILING DATE: August 10, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lori Y. Beardell
;; REGISTRATION NUMBER: 34,293
;; REFERENCE/DOCKET NUMBER: UPN-1108
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6295 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-004-311B-4

Query Match 4.7%; Score 155.2; DB 1; Length 6295;
Best Local Similarity 69.4%; Pred. No. 2,60-32;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 593 GGTAATGCGATGTCATATTTGGASAAAGTGGGAGATGCTTTTATCTAATTCATGG 752
DB 1598 GGTAAATGCGCTTAICGTACTATGATAAAGTTCTGATGGCTTTTATATGATGAATGG 1657
QY 753 GATGGAGCCATATGTAAGTCATATATGACCAATCTGCAAGAGCATGCGCCGATACCAATC 812
DB 1658 TCTGATGCGCTATATTTGACCTTAGCATCTGATGATGAAAGTGGTTCATGCTGCT 1717
QY 813 ATTTGAATCTCTGAAAACAACTTGCATGCGCATGCTTCAATTTGAAGTACTTTGAT 872
DB 1718 AATTGAATCAPTAAGAGCTGTTGATTTCTGTTGATCTTCTGCTTGAAAGCCATCACT 1773
QY 873 AGATGGGCATAGTGATGCTAGCTTAAAGAACTGCAAAACAGGGTGCCATAATATTTCTC 932
DB 1778 TCATAGCGGTAGTGATCCAGCCCTTCAAGGAACITCACAATAGAGTCCATGACATATCTG 1837
QY 933 CAGTTCTGTAAACACAAAAGAGGTTCACATCATATAGCAAAAGCTGGTATGCAATCACTT 992
DB 1838 TAGTGCATTACCAACAAAAGAGGTGTTGATCAGCTGGCAAAAGCTTATCTGCAATCGTAT 1897
QY 993 GGGG 996
DB 1898 GGGG 1901

RESULT 14
US-08-261-432-4
;; Sequence 4, Application US/0926,432
;; Patent No. 5602322
;; GENERAL INFORMATION:
;; APPLICANT: Ecker, Joseph R.
;; APPLICANT: Kieber, Joseph J.
;; TITLE OF INVENTION: Constitutive Triple Response Gene
;; NUMBER OF SEQUENCES: 13
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
;; ADDRESSEE: No. 5602322ris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: U.S.A.
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: us-09-904-389-1,432

;; FILING DATE: June 17, 1994
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/003,311
;; FILING DATE: January 12, 1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lori Y. Beardell
;; REGISTRATION NUMBER: 34,293
;; REFERENCE/DOCKET NUMBER: UPN-1864
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6295 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-261-432-4

Query Match 4.7%; Score 155.2; DB 1; Length 6295;
Best Local Similarity 69.4%; Pred. No. 2,60-32;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 693 GGTAATGCGATGTCATATTTGGASAAAGTGGGAGATGCTTTTATCTAATTCATGG 752
DB 1598 GGTAAATGCGCTTAICGTACTATGATAAAGTTCTGATGGCTTTTATATGATGAATGG 1657
QY 753 GATGGAGCCATATGTAAGTCATATATGACCAATCTGCAAGAGCATGCGCCGATACCAATC 812
DB 1658 TCTGATGCGCTATATTTGACCTTAGCATCTGATGAAAGTGGTTCATGCTGCT 1717
QY 813 ATTTGAATCTCTGAAAACAACTTGCATGCGCATGCTTCAATTTGAAGTACTTTGAT 872
DB 1718 AATTGAATCAPTAAGAGCTGTTGATTTCTGTTGATCTTCTGCTTGAAAGCCATCACT 1773
QY 873 AGATGGGCATAGTGATGCTAGCTTAAAGAACTGCAAAACAGGGTGCCATAATATTTCTC 932
DB 1778 TCATAGCGGTAGTGATCCAGCCCTTCAAGGAACITCACAATAGAGTCCATGACATATCTG 1837
QY 933 CAGTTCTGTAAACACAAAAGAGGTTCACATCATATAGCAAAAGCTGGTATGCAATCACTT 992
DB 1838 TAGTGCATTACCAACAAAAGAGGTGTTGATCAGCTGGCAAAAGCTTATCTGCAATCGTAT 1897
QY 993 GGGG 996
DB 1898 GGGG 1901

RESULT 15
US-08-003-311B-3
;; Sequence 3, Application US/08003311B
;; Patent No. 5444166
;; GENERAL INFORMATION:
;; APPLICANT: Ecker, Joseph R.
;; APPLICANT: Kieber, Joseph J.
;; TITLE OF INVENTION: Constitutive Triple Response Gene
;; NUMBER OF SEQUENCES: 13
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
;; ADDRESSEE: No. 5444166ris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: U.S.A.
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,311R
FILING DATE: January 12, 1993
CLASSIFICATION: B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/928,464
FILING DATE: August 10, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/MARKET NUMBER: USN-1108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 632 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08 003 311R-1

Query Match	4.78	Score 155.2	DB 1	Length 6312
Best Local Similarity	69.48	Prod. No. 2,600,32		
Matches	211	Conservative	0	Mismatches 93
			Indels	0
			Gaps	0
QY	693	GGTAAATGGATGGATGCTATATTTGGAGAAAGGGTCAATGGTTTAACTAAATTCATGG	752	
DB	1598	GGTTAAATGGCTGCTTATGCTATGATAAAGTTCTGATGGGTTTAAATGAAGAATCG	1657	
QY	753	GATGAGCCCATATGATGGTCATTAAGCACTAAATCTGCAAGGGAAGGGGTATACCAATC	812	
DB	1658	CTGGATCTCTATATTGGACCTTATGCTATGACCTGACCTGATGAAAGTGGTGGCATCCCTTC	1717	
QY	813	ATTGCAATCTCTGAAACAGCTTGATTCACAGATCGGTTTCATCAATGGAAGTAGTTTGAT	872	
DB	1718	AATTCGAATCAATTAAGAGCTTTTGATTCCTGGTGTGATTCCTGGCTTGAAGGCAATCAATC	1777	
QY	873	AGATCGGCTATAGTGAATGCTAGCTTAAAGAACTGCAAAACAGGGTGCATATAATTTCTTC	932	
DB	1778	GATAGGCTAGTGAATGCAAGCTTCAGGAATTCATCAATAGAGTGCACGACATATCTTC	1837	
QY	933	CAGTGGTAACTCAAAAAGGCTTGCAGATCATATAGCAAAAGCTGGTATGCAATCACTT	992	
DB	1838	TAGCTGCTATTACCACAAAAGAGGTTGTTGATCAGCTGCAAAAGCTTATCTGCAATCGTAT	1897	
QY	993	GGGG	996	
DB	1898	GGGG	1901	

Search completed: October 22, 2002, 10:42:30
Job time: 125 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

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Run on:      october 22, 2002, 09:59:55 ; Search time 60 Seconds
            (without alignments)
            1573.545 Million cell updates/search
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File #: US-09-404-389-2

Perfect score: 4435

Sequence: 1 MEMGRRSYSLISQPIEF...KPMIKQAPQSPSTGFLSV 850

Scoring table: BLA)SUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 s

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12:	/\$TDS1/genedata/hold/geneseq/geneseq-emb1/AA1992.DAT *
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17:	/\$TDS1/genedata/hold/geneseq/geneseq-emb1/AA1996.DAT *
18:	/\$TDS1/genedata/hold/geneseq/geneseq-emb1/AA1998.DAT *
19:	/\$TDS1/genedata/hold/geneseq/geneseq-emb1/AA1997.DAT *
20:	/\$TDS1/genedata/hold/geneseq/geneseq-emb1/AA1999.DAT *
21:	/\$TDS1/genedata/hold/geneseq/geneseq-emb1/AA2000.DAT *
22:	/\$TDS1/genedata/hold/geneseq/geneseq-emb1/AA2001.DAT *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	8		Length	DB	ID	Description
		Query Match					
1	2742.5	61.8	821	16	AAR80574	Arabidopsis CTRL p	
2	2742.5	61.8	821	18	AAW17938	Constitutive tripl	
3	2742.5	61.8	821	22	AAB50438	Arabidopsis thalia	
4	2738.5	61.7	821	15	AAR46723	Arabidopsis thalia	
5	1250	28.2	933	22	AAB50437	Arabidopsis thalia	
6	1243	28.0	983	22	AAR50439	Tomato TGF2, Lys	
7	1209	27.1	903	22	AAR50440	Rice EDF1, Gly2a	
8	1127.5	25.4	970	22	AAB50443	Barley EDRL, Roid	
9	584.5	13.2	732	21	AAG45983	Arabidopsis thalia	
10	584.5	13.2	760	21	AAG45982	Arabidopsis thalia	
11	570	12.9	599	21	AAC45981	Arabidopsis thalia	

THE FUTURE OF THE FUTURE

RESULT 1
AAE80574

11. AARE-74 standards, Project 1, 8-1 /A.

A.A.C.U. 74;

19 JAN 1995 (TUESDAY)

Antibodies to viral protein.

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PN
XX
US4441007A.

PD
ZZ-000-1495.
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PF
XX
10-AUG-1992; 9205-092840

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PR 12-JAN-1993; 9305=000331
PR 10-AUG-1993; 0017=0003846
PR 10-AUG-1993; 0017=0003846

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FOR OFFICIAL USE ONLY

[illegible][illegible]

DR N-PSDB; AAQ98816.

PT New constitutive triple re

Let improved properties

[illegible]

ELISA, IgG	
AAH50437	
IT	AAH50437 standard; Protein; 933 AA.
XX	
AC	AAH50437,
XX	
DT	13-MAK-2001 (first entry)
XX	
DE	Arabidopsis thaliana EDRL
XX	
KW	Arabidopsis thaliana, EDRL, enhanced disease resistance; anti fungus,
KW	antibacterial; gene therapy; transgenic plant; pathogen

XX New gene EDRL of *Arabidopsis thaliana*, the disruption of which enhances
PT disease resistance in plants, is useful for producing transgenic plants
PT and mutants having increased resistance to plant pathogens.
XX
PS Claim 5; Fig. 2, 9ppt, English.

The present sequence is given in a specification relating to the EDRI gene located on Arabidopsis thaliana chromosome 1 between markers ATRAIL and NCC1. The disruption of the EDRI gene is associated with enhanced resistance of a plant to plant pathogens or other disease causing agents. A mutated transgene comprising the EDRI gene mutated at residue 696 of the of kinase encoding domain may be introduced into the plant genome to reduce expression of EDRI. Alternatively, a transgene that expresses part or all of an antisense strand of the EDRI gene may be introduced. A transgene which expresses a sense strand of the EDRI gene may be introduced to produce fertile Arabidopsis thaliana plants. Transgenic plants exhibiting the desirable phenotypes of lack of EDRI protein, EDRI mRNA, or enhanced resistance to plant pathogens can be used for plant breeding, or directly in agricultural or horticultural applications. Plants containing one transgene may also be crossed with plants containing a complementary transgene in order to produce plants with enhanced or combined phenotypes. EDRI nucleic acids may be used as probes to detect the presence and/or expression of EDRI genes and to identify related genes from other plant species.

XX	SQ	Sequence	933 AA;
		Query Match 28.2%; Score 1250; DB 22; Length 933;	
		Best Local Similarity 34.7%; Evid. Rot. 20-106;	
		Matches 315; Conservative 128; Mismatches 277; Indels 189; Gaps	
Q7	80	SSLSSDYATITLSHPAANEINALEYILHDTFVPMKAVGSSNNSTKFWANCTFEESTQLQGP 145	
Db	57	SSMASP--APTAASNRADYMSS-----EEYQVQIALAISASNSGS--SEETKHKIRAA 137	
Q7	146	LVRLSSDYTCADDENMDPIDDEAALRSLSLSAFAISHRWVNDYMSYLERVPHGYLL 205	
Db	108	TLLSLGSQR-----MDSKE-----SSEVVAGRLSRQWYGVVLYVEKVVLSFY 153	
Q7	206	RMDDPVVWSLQNNLQPHCPIDSPSPKFTVDSSLPSSIFVVLIDGSLASIKELIDNRVHNI 275	
Db	154	-----DVYSLSTDSAKQGMPSLEULESNHQTPO--FEAVVNRFDHSSLHFLIFIAFT 160	
Q7	266	ESSEVIT FIVADHAKLVTHRLTEVSEFTFTFVASKPELITLLEEDMAVTLISGL 325	
Db	207	ALGOSTISVSVLVQPLARLVTEHMGSS-AEDSSIVLAFWIKSSSEKAAALNIOVPTLOEV 265	
Q7	324	SVGGGRHALLIKVLAGSILBLCKLAKADEYETELKAGSSVYAFGKKEITLGLKGRSS 383	
Db	266	KIGISFHFALLERVAQSVELPCLFVKQSHYTGNETEAVNTINLDEKELVEMIDPGI 325	
Q7	384	LCQPD-----SLNGPSSSISTSSPL 403	
Db	326	LIPALIASA--NNIVEPNSNPNKKEFLAQSNKVIKSLGSSSSGSMANYSSELRKTEA 385	
Q7	404	R-----FPRLKPIESTIDF---RELAKQVELDSOSINLVDEASSNNVSSKDAAFSVYQ 465	
Db	386	EPTSSYPKAGQPLN-IVSSPSSVTSSTQLHNS SLAIGKLRGALTEAKRIHRIYLP 443	
Q7	456	-----RLNRPDVP-----GETIVVETGLNLSLINFANQL 488	
Db	444	YNQRSEEDPRLFADRLRLKKGALPLYMIFPS--RNVILHQLGPNHLYVGGTATMMWE 503	
Q7	489	-----NQQRKSPQ-----PRSP 501	
Db	504	NYSQNEAPKKKENSYLENLPRLHRLFKYNTLSQATGSGFMDALSGVYHRLRYTVYH 563	
Q7	509	VASPYSVOST-----PVENVV-----PESHSLGSPSESH 538	
Db	564	VAVPSSETSTENGFRPSIVLPMNNTNNITDQPHTAAVVLEKMLSHLHKKYLSGL 623	
Q7	624	ITATGRPM-CHVNNIFVHGSQLLEETNEL-SLGLDLVLPWTLDEKLGAGSEGLV 691	
Db	624	ISTGOLPELKDHSTSSSDSTSYPNDPQVLDAVGECEIPWNIIVIAKIGLSYGEV 683	
Q7	692	YEGTWKSTVAVEILLTDHIFKVNTELELVAIMESLEHRLVITMVALETINLSIV 761	
Db	684	YHADWRTGEVAVKKFLDQDSGAALAEIKSEVKIMRELRKHPNVVTHLAAVNTINLSIV 743	
Q7	752	EYLSQCEIYVITKESGVETPTETFINMATTVAFMMVIRHSPVAVHSPKSERILAE 811	
Db	744	EPLPGELYKILHQP KSHLSEKELFPMALIVAMVMNS--HPTETTVAGS--ETPRILAVN 802	
Q7	812	EYIVEVCEITLSELEAKTELSKLAAGTITWZATGVLEHETPRERKNTVNTVLLKELAI 871	
Db	803	NNNVKVCDFULSPLEKNTHTSSKSTAGIPKWMAPFVLEHETPSNPKGLAVSPVILWELAI 862	
Q7	872	GLTWVNIQAQVVAAVTEKCEKLLITPTFVNPFLASIVA--WAGTFKPGSTFGLMELE 931	
Db	863	LHLPWEGMNMQVVGAVGFGQGNRIETPKETDPVVRIRITITFWETDPMKSSAQLEVLK 922	
Q7	832	PMTEQAPP 839	
Db	923	PINRLVLP 930	

RESULT 6

PD 30-NOV-2000.
XX
PF 26 MAY 2000; 2003W032814710
XX
PR 26-MAY-1999; 9905-0135895.
XX
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
PI Innes RW, Frye CA;
XX
DE WP1; 2001-025156/03.
DR N-PSDB; AAC90485.
XX
PT New gene EDR1 of Arabidopsis thaliana, the disruption of which enhances
PT disease resistance in plants, is useful for producing transgenic plants
PT and mutants having increased resistance to plant pathogens
XX
PS Claim 13; Page 81-83; 91pp; English.
XX
CC The present sequence is given in a specification relating to the EDR1
CC gene located on Arabidopsis thaliana chromosome 1 between markers
CC ATRAF1 and NCC1. The disruption of the EDR1 gene is associated with
CC enhanced resistance of a plant to plant pathogens or other
CC disease-causing agents. A mutated transgene comprising the EDR1 gene
CC mutated at residue 636; 11% of kinase encoding domain may be introduced
CC into the plant genome to reduce expression of EDR1. Alternatively, a
CC transgene that expresses part or all of an antisense strand of the EDR1
CC gene may be introduced. A transgene which expresses a sense strand of
CC the EDR1 gene may be introduced to produce fertile Arabidopsis thaliana
CC plants. Transgenic plants exhibiting the desirable phenotypes of
CC lack of EDR1 protein, EDR1 mRNA, or enhanced resistance to plant
CC pathogens can be used for plant breeding, or directly in agricultural or
CC horticultural applications. Plants containing one transgene may also be
CC crossed with plants containing a complementary transgene in order to
CC produce plants with enhanced or combined phenotypes. EDR1 nucleic acids
CC may be used as probes to detect the presence and/or expression of EDR1
CC genes and to identify related genes from other plant species, such
CC as the gene from Oryza sativa that encodes the present sequence.

XX Sequence 903 AA:
SQ
Query Match 27 18; Score 1200; 22 22; Length 903;
Best local similarity 34.1%; Pred. No. 8,50-102;
Matches 304; Conservative 122; Mismatches 224; Indels 236; Gaps 22.
QY 170 AALPSLSISAEASHPEFWVWNGMSYLERKVPDGFYLLHGMDFYVWSELCTNLQEDQRPSPSE 229
DB 17 AAVRDFQTADALSPRYDYNEFDYHEKVVDGFYDFG--PSMES-----SKQKMPSLA 69
QY 230 SLKTVDSISGSSLEWVLIDRHSASLKLQN-----RVNINSSSCVTTKEVADHIA 280
DB 70 DLQDTGDTGCG--PFTVTVNPAIDFTIQEMEQAQCTIIIDFPVANIAA-----LVQRIA 120
QY 281 KLVNHLGGSVSRFPDIIVSARKESDOLKECLGSAVLPGLSLSVGLCRHALLFKVLAD 340
DB 121 ELAVTDHMGPKVDA-NMLTRWLEKSTELRTSLHTSLPFGICIKGLSRHALLFKILAD 179
QY 341 SIDLPCKRIAKGCKYCTETPLASSCLVKEGLDRHYLLDILGKPGCLQCPDLSLLNGPSSISIS 400
DB 180 SVGLPCKLVKGSNYTGDDDAINIKMN-EREFLVLMMAAPGTLPISDVLSWKGNLSIN 238
QY 401 SPLRFPRLKPIESTID-----FRS-----LAKQYFLDSQSLNLVFE 437
DB 239 AKLTQNPVLAGSSSTTUSHLNANALFPVGHKQQQLPSSGFWILASQSEYKGTGATTSSQA 298
QY 438 ASSG- NVVSEKDAEFSYICR ---PLNEK-EVDGKT 467
DB 299 SSSGTTVAAGSAFSSSWTVSHQSDSDPSTSAQMSAQKVIIQGEHPWNNINAPNEN 358
QY 468 IVVTGDKORNSQLN-----KKAQLNTQCKSRQPP-----SCVASPYSVQ 509
DB 459 IRLVSDIQCNSSEINIFAPINFPVGRPKFTFVPLNFPNPNENELQFRFENVVVPTFSPQ 418

QY 510 STPFVENVPLSHIS-----HIGSE----- 561
DB 419 QELVMPHMETYILVSNKQYNYVITGAPQYSGAGSSAVATFARTRIRVAVRIRI 478
QY 532 EHLLA-----LSHERM 542
DB 479 FYMAAHNTNSMASSEAMKMTSTAGICKVKEVKNVNDLKLINSELDHGFILHKKWIR 508
QY 543 -----DIVNNLP-----FVHNSLLIKRNFELIS 560
DB 539 SVLTPPTLVARQALHKESEITLGGPFAH-----KME----- 562
QY 567 -----LEDLVIPWTDLDLPEKIGAGSEFIVYRHWESIVAVKILIEQDFHPE 614
DB 599 ARSHKLQIMEDVSECETHWEDLVICERIDCSYCYVKAWNDEIVAVVEFLIQDFYED 658
QY 615 RVNEFLREVAIMKSLKHENIVLFMGAVIKPPNLSIVTYLSKGSIVYRLHKSQVKIDDEI 674
DB 659 ALDEEFSEVPIMPFIPHNIVIFMCAVTEPPNISVETIKESIVYRHKPNQV 717
QY 675 FETAMAFVAREEMRIHKEFEPVHSGESENIVYEFIVAVVAVVAVVAVVAVVAVV 704
DB 718 FETAMALLVAREEMRLHLSVITVHETLESINLAVRRWAVEVTEVLSKSRHATVET 777
QY 735 SAATTEWMAFEVLEFENEKSEVSEVLEKELALGCEWTRNKAQVAVAVVAVVAVV 794
DB 778 SIATTEPMAFEVLENEKSEKTVSYFVGVINFIATLEMWSESMENMVAVVAVVAVV 847
QY 795 LQPPFVNPGLASIVACWADEPWKRKPSFSSIMEILKPMIKQAPF--QDSRT 844
DB 838 LDIPKEIDPLVARIWECWQGDPNLPSPFAQLISALFTVQRIVTFPSHSPSS 889
RESULT 8
AAB50443
ID AAB50443 standard, Protein, 970 AA.
XX
AC AAB50443;
XX
DT 13-MAR-2001 (first entry)
XX
DE Barley EDR1.
XX
FW Barley, EDR1, enhanced disease resistance; anti-fungal;
KW antibacterial, gene therapy; transgenic plant; pathogen.
XX
OS Hordeum vulgare.
XX
PN W0200071696-A1.
XX
PD 30-NOV-2000.
XX
PF 26-MAY-2000; 2000W0-0514718.
XX
PR 26 MAY 1999; 9905-0135895.
XX
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
PI Innes RW, Frye CA;
XX
DR WP1; 2001-025156/03.
DR N-PSDB; AAC90486.
XX
PT New gene EDR1 of Arabidopsis thaliana, the disruption of which enhances
PT disease resistance in plants, is useful for producing transgenic plants
PT and mutants having increased resistance to plant pathogens
XX
PS Claim 13; Page 85-87; 91pp; English.
XX
CC The present sequence is given in a specification relating to the EDR1
CC gene located on Arabidopsis thaliana chromosome 1 between markers
CC ATRAF1 and NCC1. The disruption of the EDR1 gene is associated with
CC enhanced resistance of a plant to plant pathogens or other

CC disease-causing agents. A mutated transgene comprising the EDRL gene
CC mutated at residue 696 of the 696 amino acid coding domain may be introduced
CC into the plant genome to reduce expression of EDRL. Alternatively, a
CC transgene that expresses part or all of an antisense strand of the EDRL
CC gene may be introduced. A transgene which expresses a sense strand of
CC the EDRL gene may be introduced to produce fertile Arabidopsis thaliana
CC plants. Transgenic plants exhibiting the desirable phenotypes of
CC lack of EDRL protein, EDRL mRNA, or enhanced resistance to plant
CC pathogens can be used for plant breeding, or directly in agricultural or
CC horticultural applications. Plants containing one transgene may also be
CC crossed with plants containing a complementary transgene in order to
CC produce plants with enhanced or combined phenotypes. EDRL nucleic acids
CC may be used as probes to detect the presence and/or expression of EDRL
CC genes and to identify related genes from other plant species, such
CC as the gene encoding the present sequence from barley.

XX
SQ Sequence 970 AA:

Query Match 25.48; Score 1127.5; DB 22; Length 970;
Best local similarity 32.18; Pred. No. 5.2e 95;
Matches 495; Mismatched 133; Mismatches 272; Indels 243; Gaps 24;

QY 94 APTLSNP--AANFINAI EYIIIDDFVVMKAVASVSSSKSWAQOTFSPQIQPIVLPSS 152
Db 37 APSRPPVASTEAAGDEFLQ-----EEYQMQ--LALALSA 71
QY 153 DXTCADDPNEMDPIIDP-----AALRSL-----SISAEAISHRFWVNGCMSYLE 196
Db 72 SASAGAGAG--DPPGFGIRKAKIMSLQKPPV--NRPICGYATASISPPYFYRIPLNYE 129
QY 197 KVPDGFYLIHGMIDPVVMSLCTNLQEDGRIPSESLKIVDSSIGS--STEVLLIDRHSBASL 255
Db 130 KVTDFEYDFPDP-----AFSGHDFP--SLARLMSIGLGYEVIVVDYKIDNAL 179
QY 256 KFLQNRVHNISSSGVTKFVADPHIAKIVCNHIGSVSEGEDLVSAWKEGSDDLKECLQS 315
Db 180 QEMKEVAFQCIIGQPIITVIVPPIAEVVADEMAGPVIDA--NEMITPWLKSTEQRTSHQT 238
QY 316 AVIPLCSLSVGLGRHRAILFKVLADSIDLPCR AKGCKYCTPDGASSCLVPFGLDREYLI 375
Db 239 SLTHIGSTETGISRRATLEKTIADMGVLPCKIKESHYTGVEDAINIKRMNKRREPLV 298
QY 376 DITGPQGTGQPSLINCPSISISUSPIREPRLKPIESTIDERSLAKQ-----YEL 426
Db 299 DVMAAPGTLIPADVNSKGTPTNFSTQIQNQVVSASNIEDDPVALQSEHEHYQGIMFA 358
QY 427 D--SOSLNI VPEASSGNVVS-----GK-----DAAPSV 453
Db 359 NDRVSDNLSSTENTMTAGSSASEFGTLGKAS--LAGAFSKQKKNLQIIPDSHEIDERSNL 418
QY 454 YQY--DINRNVNDEFTIVVTQEDENICQLNKA 485
Db 419 FAEDDPENATESKSSIAFKGLNNRNSDFRRPENVVPPSARSQPIVXKNWSACNDISN 478
QY 486 -AQLNTQDG-----KSEQFRSCVASPTYSVQSTPFVE----- 515
Db 479 RQZRVVAPSVFPEFNATENASGSLAALSTAEIYN PNVEELNERYAALNYDNKI 534
QY 516 -----NVVPLSHITIGSED----- 530
Db 535 LQTSAMAKASTGCTHARSQVTPGLYYDKMLGTSSMNIASSSGIGKVAEKDQNDLEKQPI 594
QY 531 -----SEHLLALSHPRMDHVNLL-----PFVHGSQLIR-----KPN 561
Db 595 YSRFDGELSKNAQGFPTFPDEHKFTNRYDHPMLIDPPPKSPLEDFEEMEPFQNIETVSPS 654
QY 562 ELSLGLIEDLV-----IPWTDLDRKIGASFGTIVYGEWHGSDVAVKILDTQDHPH 613
Db 655 QVQSSKVDIVIVDFVSGCTILWEDLVIDERIGISYGVYHADWNGTEVAVKRLDQEPYG 714
QY 614 ERVNIETREVAIMKSLREHNIIVLPMGAVTKFPHLSIVTEYLSGSSLYELHKSQVKDIDE 673
Db 715 DALDEFPRQVRIRRIEHNIVLPMGAVTERPHLSIVSEYLPFGSLYELHRENGQ-IDE 773

QY 674 TRRISMAITVARMMVLEHRETTIVHRELEHSDVWREKVVYVETIIEDEIKAPITLSS 733
Db 774 KRRIEMALLVARQMN--LHTEVPLIVHRELEHSDVWREKVVYVETIIEDEIKAPITLSS 733
QY 733 EKAATTEEMMAIVIKLEENREKTVVTVVTVVWELALITLWVNIENLAAVAAVHKK 792
Db 833 KSLAGTPEEMMAIVIKLEENREKTVVTVVTVVWELALITLWVNIENLAAVAAVHKK 792
QY 794 KCHTFEYVNEELASLIVA--WALTEWELTCLLMLMMAAMERKQAFLEQET 844
Db 864 KLTTEKIVNIVASTIKAGWKKDRHKKKILQGLATIKKIKHLEIVLHLEI 944
RESULT 9
AAG45983
ID AAG45983 standard; Protein: 742 AA.
XX
AC AAG45983;
AX
DI 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SRQ 11 Nov 1999;
XX
KW protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression; contig; protein
KW termination sequence;
XX
QC Arabidopsis thaliana.
XX
PN RP103405-A2.
XX
PD 06-SEP-2000.
XX
PR 25-FEB 2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 990S-0121825.
PR 05-MAR-1999; 990S-0123180.
PR 09-MAR-1999; 990S-0123548.
PR 23-MAR-1999; 990S-0125788.
PR 25-MAR-1999; 990S-0126264.
PR 29-MAR-1999; 990S-0126785.
PR 31-APR-1999; 990S-0127462.
PR 06-APR-1999; 990S-0128234.
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PR 16-APR-1999; 990S-0129845.
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PR 23-APR-1999; 990S-0130510.
PR 23-APR-1999; 990S-0130891.
PR 23-APR-1999; 990S-0131449.
PR 30-APR-1999; 990S-0132048.
PR 30-APR-1999; 990S-0132407.
PR 04-MAY-1999; 990S-0132484.
PR 05-MAY-1999; 990S-0132485.
PR 06-MAY-1999; 990S-0132486.
PR 06-MAY-1999; 990S-0132487.
PR 07-MAY-1999; 990S-0132863.
PR 11-MAY-1999; 990S-0134256.
PR 14-MAY-1999; 990S-0134218.
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PR 19-MAY-1999; 990S-0134941.
PR 20-MAY-1999; 990S-0135124.
PR 21-MAY-1999; 990S-0135353.
PR 24-MAY-1999; 990S-0135629.
PR 25-MAY-1999; 990S-0136021.
PR 27-MAY-1999; 990S-0136392.
PR 28-MAY-1999; 990S-0136782.
PR 01-JUN-1999; 990S-0137222.
PR 03-JUN 1999; 990S-0137528.

PR 04-JUN-1999; 990S-0137502.
PR 07-JUN-1999; 990S-0137724.
PR 08-JUN-1999; 990S-0138094.
PR 10-JUN-1999; 990S-0138540.
PR 10-JUN-1999; 990S-0138847.
PR 14-JUN-1999; 990S-0139119.
PR 16-JUN-1999; 990S-0139452.
PR 16-JUN-1999; 990S-0139453.
PR 17-JUN-1999; 990S-0139492.
PR 18-JUN-1999; 990S-0139454.
PR 18-JUN-1999; 990S-0139455.
PR 18-JUN-1999; 990S-0139456.
PR 18-JUN-1999; 990S-0139457.
PR 18-JUN-1999; 990S-0139458.
PR 18-JUN-1999; 990S-0139459.
PR 18-JUN-1999; 990S-0139460.
PR 18-JUN-1999; 990S-0139461.
PR 18-JUN-1999; 990S-0139462.
PR 18-JUN-1999; 990S-0139463.
PR 18-JUN-1999; 990S-0139750.
PR 18-JUN-1999; 990S-0139763.
PR 21-JUN-1999; 990S-0139817.
PR 22-JUN-1999; 990S-0139899.
PR 23-JUN-1999; 990S-0140353.
PR 23-JUN-1999; 990S-0140354.
PR 24-JUN-1999; 990S-0140645.
PR 28-JUN-1999; 990S-0140823.
PR 29-JUN-1999; 990S-0140991.
PR 30-JUN-1999; 990S-0141287.
PR 01-JUL-1999; 990S-0141842.
PR 01-JUL-1999; 990S-0142154.
PR 02-JUL-1999; 990S-0142055.
PR 06-JUL-1999; 990S-0142390.
PR 08-JUL-1999; 990S-0142803.
PR 09-JUL-1999; 990S-0142920.
PR 12-JUL-1999; 990S-0142977.
PR 13-JUL-1999; 990S-0143542.
PR 14-JUL-1999; 990S-0143624.
PR 15-JUL-1999; 990S-0144005.
PR 16-JUL-1999; 990S-0144085.
PR 16-JUL-1999; 990S-0144086.
PR 19-JUL-1999; 990S-0144325.
PR 19-JUL-1999; 990S-0144331.
PR 19-JUL-1999; 990S-0144332.
PR 19-JUL-1999; 990S-0144333.
PR 19-JUL-1999; 990S-0144334.
PR 19-JUL-1999; 990S-0144335.
PR 20-JUL-1999; 990S-0144352.
PR 20-JUL-1999; 990S-0144632.
PR 20-JUL-1999; 990S-0144884.
PR 21-JUL-1999; 990S-0144814.
PR 21-JUL-1999; 990S-0145086.
PR 21-JUL-1999; 990S-0145088.
PR 22-JUL-1999; 990S-0145085.
PR 22-JUL-1999; 990S-0145087.
PR 22-JUL-1999; 990S-0145089.
PR 23-JUL-1999; 990S-0145192.
PR 23-JUL-1999; 990S-0145145.
PR 23-JUL-1999; 990S-0145218.
PR 23-JUL-1999; 990S-0145224.
PR 26-JUL-1999; 990S-0145276.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.

13b 644 RETURN TO VISITING MIKAWAN EVROCH VIVV KILL 481

Search completed: October 22, 2002, 12:23:26
Job time : 64 secs

A:Map position: 4
A:Initiation: 280-636
C:Keywords: phosphotransferase; protein kinase

Query Match 34.7%; Score 1538; DB 2; Length 963;
Best local similarity 40.9%; Pred. No. 62672;
Matches 460; Conservative 128; Mismatches 239; Indels 154; Gaps 22;

QY 24 SSSSYVYV AAGNNVIEDEFTVFWEDVHHEINTQAYEIGHNYSWICLPHSSSSS 92
DB 152 ATSSPDSIDARSIVNIHERNIDKSDREVSCLP-RMSSESSFAGSEF-----SGTI 201
QY 83 YHD--SSLSDDYVAPTISNPAANFNAIFYIIIDHFFVMEKAVGSGSSOK SWAQUTE 138
DB 202 VDNFSNFSSTHAPETSTTHVWVKFF FVIVVRF -GGRQSLAQKSEF 269
QY 135 GYVLTQVTLAKWLSSQA - NICESVHIQSIESTSYRWFVWSGLSYSDK 296
QY 198 VMDQVYLIHMDQYVWSLQINQENRIPESPELEFVPSGLGSEFEVVIDRHSQASLKE 257
DB 297 ISDQVYSILGMDQYVILMCHNSQPKKTIQIIIIKTTTPN DTSMEVVLIDHFFHSFLKD 355
QY 258 LQNPVHNISSSQVTTKEVADPHIAKLVNHLQGSVSECEDMVSAWKEGSDNLEKELGSV 317
DB 356 LDKAKHFEYSSSNMLVLVERKIRIVAVYMDGNFQVEGIIQFPWFIVSNPLFEFEKCI 415
QY 318 IPCLSLVGLCRHRALLFKVLADSIDLPCR IAKGCKYCTRODASSCLVRG---LDREY 373
DB 416 LPGLSLFMGLCRHRALLFKKLADYIGLPCPIAPGCRCKESHQSSCLVKIIDPKLSREY 475
QY 374 LIIDLGRPGCLQCPDSSLNGPSSISLSSPLREFPRIKPIESTIDFRSLAKQYFLDSQSLN 433
DB 476 VMDLGRPGNVHDPOSSINGETQQLPSPLOMSHL----- 510
QY 434 VFDEASSGNVVSQKDAAFSVYQRPINKEKDVIAKTIIVTGTGKIDNSQLNKKAQINTQD 493
DB 511 -----IDPSRDVHSTSPQTV-----FKRTSPILSENIDQSSSQG 547
QY 494 KSEQF-----RSCVASPYSVQSTPFENVVPIISHISGSD-----S 531
DB 548 VRRFELPQNAQTVCAHIDQIQAKVSSMVLIESVLKALPDP-IPNLSSEKIAQQLCK 606
QY 532 EHLIALSHP-----RMDHVNNLPEVHGSQLRKPNHLSLGLDLVI 572
DB 607 EEIVLLEDPTAMKQPNLSVEFTVFAITKRRKGRPLVGLATSPYL--TTPEPLASDMLEV 664
QY 623 PWTDIDPRKICANSPQTVYRHWESDVAVKILTEQDFHPRVNEFLER---VAIMK 627
DB 665 SWNPTRKERVCAASEPIVHPAFWGSQVAVKILISQDFHIDQGPPEFIFVVFQAVAIMF 724
QY 628 SLRHNPVILFMGAVTEKPNLSIVTYLSRGSLEYELHKSGVKD-IDETPRINMAFDV--- 683
DB 725 RVRHNPVILFMGAVTERFRLSITTYLPRGSLFRLIHRPASGELLDDQRRRLRMALDVVCA 784
QY 684 AKGMNYLURKDPETVHRDLKSNLIVLKKYIVAAVDFGLSRUKAKELSSKSAAGT 739
DB 785 IPRYAKGLNYLHCLNDPPVVVHDLKSNLIVLKNWIVKVDLGLSRKANILPSKSVAGT 844
QY 740 PEWMAPEVLDERPSNEKSDVYSPGVILWELALIQPPWCNLPNPAQVVAAVGPKKPLDIPR 799
DB 845 PEWMAPEFLRGEPTNEKSDVYSGVVLWELITIQPPWNLSPAQVVGAVAFQNPPLIIPP 904
QY 800 IWNPKIASIIVACWADEPWRPEPSSIMELFPMIKOAPPO 840
DB 905 NTSIVLSLMEACWADEPFSQRPAPRSIVDTLKKLIK SPVO 944

RESULT 4
T00726
probable serine/threonine-specific protein kinase (mouse-ear cross)
C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 12 Feb 1999 #sequence_revision 12 Feb 1999 #text_change 24 Oct 1999
C:Accession: T00726
R/Shinn, P.; Buchler, E.; Dewar, K.; Ford, J.; Kim, C.; Lee, Y.; Sun, H.; Young, A.
et al.; A.; Becker, J.R.
Submitted to the EMBL Data Library, April 1998
A:Description: Genomic sequence for Arabidopsis thaliana (mouse-ear cross)
A:Reference number: 214200
A:Accession: T00726
A:Status: Translated from DB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 151015 (511)
A:Cross references: EMBL:AC003981; NIDB:4063438; PIR:4063438; GenBank:U00726
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 1
A:Map use: 214200
C:Keywords: phosphotransferase; protein kinase

Query Match 28.2%; Score 1250; DB 2; Length 1510;
Best local similarity 34.7%; Pred. No. 439067;
Matches 315; Conservative 128; Mismatches 277; Indels 188; Gaps 150

QY 86 SSSSYVYVAPTISNPAANFNAIFYIIIDHFFVMEKAVVSNVSGKSWAQTEFLQQLP 145
DB 139 SSMAAP--APTAASNRAIDYMS--FFYQVQALIA SASNSQS SDQRRKQKRAA 189
QY 146 LVILSSDXTCADDPNEMDPIIDEAALPSLSISAFATSHRFVWNGMSYELKVPIDGFLY 205
DB 190 TELSLASHQF-----MDSRP-----SSEVVAQPSLQVWEYGVLYDFKVVLSFY 245
QY 206 RCMVYVWVETINCLQCFLESTFSLVIVSLEETEVVLTFHSTAS-PRHKNVENI 265
DB 236 ----DVSLSIDSAKQGEPSLEIDLESNCHGFG--FEAVVVRNLTSSSHLELTAET 288
QY 255 SSSVVT--KEVAPHIAKLVNHLQGSVSECEDMVSAWKEGSDNLEKELGSVAVIPLSL 323
DB 289 ALGQSTTSVSVLVQLAELVTEHMGSS-APNLSIVIARWIEKSSSEPKAALNIVVFIQEV 347
QY 324 SVSLGRHRAALLFKVLADSIDLPCR IAKGCKYCTRDPASSCLVREGLDREYIIDLGRSP 383
DB 348 KIGISGHRKALLFKVLADSVRLPCRKLVKSHYIGNEDDAVNTIRLEDEREYVILMDIPL 407
QY 384 LQDPD-----SLNNDSSISSTSI 408
DB 408 LIPALFASASNNIVEPCNSNGNKFTAGLSNVIKLSGGLASGSSMANTSSSLGRKLEA 467
QY 404 ----PDPVQVPESTIDE--PSTAPAVPEISQSLNIVAVGAGAGSNVVSRLAAAFSVY 466
DB 468 ERHSSYFKVGLPN-IDYSSPSSVSSIQLENNSS-LATGR KSGALVLRKNNNIVP 525
QY 456 -----FLANSEVQ-----GRVIAVPRKPRNPLNPLNPLAAAL 488
DB 526 YKQNSLEEFENLIADNPFQNGKAGAEKLYMETESQNNVIVHLENNPQVDSALMKKK 585
QY 489 -----NIQDKSEQ-----FKSP 611
DB 586 NYSNLIAPKKKNSYTERLLIKLRDPKRYQNTQQVATSSGRLATSGVHDKNVLEVSF 645
QY 502 VASYSVQST-----PEVENVV-----PISHSSTHSESEB 683
DB 646 VAVPSSPTSTENQRPSPSIVEFMNNTNNILNQHITAADVHVDQNDSESHHGRKYSIDP 745
QY 534 ELALSHPRMTHVNNLPFVHGSQLRKPNHLSLGLDLVLPWIDLERKQAGSEFTV 691
DB 706 ISTGVDPRLKDHSTSSSLDSTSYRNDPQVILIDAVAGECTPWNDLVAPKRLGASVYEV 759
QY 592 YRGEWRGSDVAVKILTEQDFHPRVREFLPEVATMKSLRHNTVLPWMAVTEPNLSIV 691
DB 766 YHAIWHGIEVAVKFLIQDFSGAALAEKRSVAKIMKIRKPNVVFELAVTEPNLSIV 725
QY 652 TVYVDSSTVYTHFSSVETITETESTRMATLVAFEMDTEHREFTVMDPTEPLATEK 711
DB 711 ----- 711

Db 297 DEWMAPEVLNRNEPANKEKCDVYSGVITWFIATSPVQWKCI NPMQVVCAVGQPNRPI F14P 356
QY 800 IYNPKLASLIIVAWADEPWKRSESSIMELIK 831
Db 357 DIDLIVAQTIIEKQWQIEPHLRPSFTQIMQSLK 388

RESULT 10

F96701

protein kinase homolog F7H19.240 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 23-Apr-1999 #sequence_revision 23 Apr 1999 #text_change 23-Jul-1999

C:Accession: F96701

R:Reagan, M.; Peters, S.A.; van Staveren, M.; Dirksen, W.; Stickema, W.; Banerjee, I.; Mew

submitted to the Protein Sequence Database, July 1998

A:Reference number: Z15399

A:Accession: F96701

A:Molecule type: DNA

A:Residues: 1736 (REV)

A:Cross-references: EMBL:AF031018

A:Experimental source: cultivar Columbia; BAC clone F7H19

C:Genetics:

A:Map position: 4

A:Introns: 1167 (REV) 4773 4773 5193 5472 5734 6033 6233 6433 6633 6833 7033 7233 7433 7633 7833 8033 8233 8433 8633 8833 9033 9233 9433 9633 9833 10033

A:Note: F7H19.240

Query Match

Best Local Similarity 42.0% Score 806, Db 2, Length 736

Matches 170; Conservative 72; Mismatches 135; Indels 28; Gaps 7;

QY 457 PLNKEIVTGETIVTGERKNGALLNEEAA₂INTLQKSTLPSVASFYSVQSTPIVVEN 516

Db 426 PLKRNIN KSAAGGGSGSASAAVITATRN 274FFPAVPLSAVGNCAALAHIN 384

QY 517 VVPLRHLHLRRE 388HLCALQFEMCHVRN 114V 81534

Db 583 GDSLTIONLQSKPTRELLSALVSMRTEFMSTIRVITFANPLSLSVTEFLILAVNS 412

QY 574 SGL 388RNRNLTIVTWTITITIKELANSTVTVGQHWPSIVAVEILIEIE 611

Db 445 KQSPVNRKRRFVH 277SWET 426EYVDEPTAAVHGVNSIVAKVTITIC 502

QY 612 HDEPVNTEPRVAMER 589PVVITWAVTTPR 21VTTTPE 25VETLHKSTVET 671

Db 503 NAMLTCEKKEFINMKR 600NVITFM 50VAVTEESALIMEYPRSEIEFLHNIN 561

QY 672 DETRETNNAIVAKEMNTLHRSKFIIVSGASFNHAKYRIIVAVWEGEGSEKAFIEI 731

Db 562 DKKKEIFMALIVAKEMNYDEKNGEIVHRLK 581VIFNSVVPVGVPTKAWNATIT 620

QY 732 GFEVAAV 211VWAG 210 388RNRNLTIVTWTITITIKELANSTVTVGQHWPSIVAVEILIEIE 611

Db 622 SPKSGKGTFOWMAPVLRSEKSDVPSGVILWELMTTIVPWDRKLNSTQVGVGVGM 681

QY 792 GKPLVPRVNPRLASLIIVAWADEPWKRSESSIMELIKPMTKQ 836

Db 682 DSRRLDPEGINPRIASIIHSGWQIEPAKRSIHLISQMSILRK 726

RESULT 11

F96701

hypothetical protein T24K23.26 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: F96701

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Guen, L.; Conway, A.R.; Ganway, A.R.; Greasy, T.H.; Hewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 409, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, F.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lures, J.S.; Magill, R.; Marshall,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.E.; Shinn, P.; Southwick, A.M.; Tan, R.; Tallon,

Db 172 POLSIVIEYMSIGSYVIVL-RISQKFFISWQFKIKIAPICPQIMYIRKMG--IVRPNITS 228
QY 706 PNLIVIRKFTYVKKVGGESKFAEELSSKSAAGTITPEWMAQAVIKRPPSNEKSDVYSFGV 764
Db 229 ARGLNKEF IVKIVTIGLTERMGIAVFI TEAAATTEWMAHLIRRIIVTEKSGTYSFGV 287
QY 765 ILWELATLQQPWNLNPAQVVAAVGGPKKKKLDIPROVNPKLASLIVACWADNPWKRPSPFS 824
Db 288 LMWELATLSEKPFVYFEFEVIRIVANIRARLEITFG -PAGELIALEWQSLRGEKISGR 343
QY 825 SIMETLIK 831
Db 344 RILHKKK 350

RESULT 15
D84555
probable protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84555
R:Lin: X.; Kaul, S.; Rounsley, S.D.; Shen, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, I.; Tallon, L.;
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; M81D:2008487
A:Accession: D84555
A>Status: preliminary
A:Molecule type: DNA
A:Restrict: 1-546 sSite
A:Cross-references: GB:AE002093; NID:q6598802; PIDN:AA80785.2; GSPDB:GN00139
C:Genetics:
A:Gene: A12417700
A:Map position: 2

Query Match 13.2%; Score 584.5; DB 2; Length 546;
Best local Similarity 30.6%; Pred. No. 5,1e-23;
Matches 166; Conservative 82; Mismatches 175; Indels 119; Gaps 16;

QY 439 BRALLKFKVLAD SIDLPRKIAKCKYCTEDAGSELVETGLRHHYLLDLIG 379
Db 84 HQRLI KLAADPATRPVFEVRSVQVSPKISADSDPAVEEDAQSSHPSG----- 131
QY 480 RFGGLQCP-----DSSLNGPSSISISSPLRPPLKPIESTIDPR 418
Db 132 PGVLAPPTFGSSPNFEALTGSKIVIEWVSVVNATLSTRPMHETP-----STIDKP 183
QY 419 SLAKQFELESGSTNAVETEASNNVSSGEAAFSVYLRPNFALVGLALVVIG----DA 474
Db 184 KLLSQITSLIGELGLNIQEAHAFSTVG----FSL-----DV----FVVDGWSQRET 227
QY 175 PENQQLINPKAAALNTQKYSRPFSSGVAVSYVSTPTVENVVPLSHIGHIGSEDSEHL 534
Db 228 DGLKDALSKETLLKLDQPGSKQ-----KSI SFFEH-----DKSSNEL 264
QY 535 LAUSHPRMHHVNNLPVVHGSQTRKFNPLCHGELTIVFWTHLIRKKLGASFGTVYRG 594
Db 265 L-----PACIEIPIID--GTDEWEIDVTQIKRKKVASGSYGDILHRG 303
QY 695 FWRGSDVAVPFTTFQDPHPRVPRHLPRVVAIRKTELEHNPVILRMGAATKPPHLSIVTEYL 654
Db 304 TYQSGEVAITKELKDDRVNNFMIRFSGQVFIMPKVFHKNVVQFEGACTRSPPTLCIVTFEM 363
QY 656 SRGSLVLELHRSGVETLEIRFENMATVAKGMNYLHEKEITLVHDEKCTINLAVLKRYT 714
Db 364 APQSTVYVPIHFQVAVVETLIRKVALVAKGMVYILPRG -IRGGLKIAKLMLERGL 420
QY 715 VKVGLDGLSLRKLKARTFLSSKSAAGTFEWMAPFVLEIRDPSPNEASDVYSFGVILWELATLQQ 774
Db 421 VKVALPQAVARVQIESGVMT-AETISTYRWMAPEVLEHKPYNHKADVFSAIVLWELLTGDI 479

QY 375 FWRGSDVAVPFTTFQDPHPRVPRHLPRVVAIRKTELEHNPVILRMGAATKPPHLSIVTEYL 654
Db 480 PYAFLLPQLQAAAGVVQKGLRPAITKALIDFKVAGLLERQWHKQDPEQRILLEBELLEMLAQILM 544
QY 835 KO 846
Db 540 KE 541
Searched, completed: October 22, 2002, 14:22:20
Job time : 48 secs


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RX MEDLINE 92419540; PubMed/1620546;
KA Eychenne A., Garnier J.V., Desrosier R., Maza M., Lantier P.,
KA Calogeraki T., Calothy G.;
RT "Quail neuroretina c-Rml(B-raf) proto oncogene cDNAs encode two
RI proteins of 93.5 and 95 kDa resulting from alternative splicing.";
RL Oncogene 7:1315-1323(1992);
CC 1 FUNCTION: MAY PLAY A ROLE IN TRANSDUCING SPECIFIC SIGNALS IN
CC NEURAL CELLS.
CC 1 CATALYTIC ACTIVITY: ATP + a protein ADP + a phosphoprotein.
CC 1 SUBCELLULAR LOCATION: Nuclear.
CC 1 ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC 1 TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL TISSUE.
CC 1 PIM: PHOSPHORYLATED.
CC 1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MIL/RAF SUBFAMILY.
CC 1 SIMILARITY: CONTAINS 1 ZINC DEPENDENT PHORBOL ESTER AND DAG
CC BINDING DOMAIN.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/seq/seq.htm
CC or send an email to license@isb.ch).
CC -----
DR EMBL: M80846; AAA49493.1;
DR EMBL: M80845; AAA49492.1;
DR HSSP: P04049; LEAK.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR00719; Euk_pkinase.
DR InterPro: IPR004116; RBD.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; DAG_PE_bind; 1.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF02196; RBD; 1.
DR PRINTS: PR00038; DAGPEPEMAIN.
DR SMART: SM00109; C1; 1.
DR SMART: SM00455; RBD; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00102; PROTEIN_KINASE_ST; 1.
KW Protein kinase; transferase; Serine/threonine-protein kinase;
KW ATP binding; Nuclear protein; Alternative splicing; Zinc;
KW Phorbol-ester binding; Phosphorylation.
FT DOMAIN 1-2 129 POLY-SER.
FT DOMAIN 245 280 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 248 280 CYS-RICH.
FT DOMAIN 497 757 PROTEIN KINASE.
FT NP_BIND 503 511 ATP (BY SIMILARITY).
FT BINDING 523 523 ATP (BY SIMILARITY).
FT ACT_SITE 616 616 BY SIMILARITY.
FT VARSPLEN 392 432 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 807 AA; 89521 MW; 1F9700A95242B7 CRC64;
Query Match 10.4%; Score 462; DB 1; Length 807;
Best Local Similarity 39.3%; Pred. No. 1; Lc 22;
Matches 110; Conservative 50; Mismatches 97; Indels 14; Gaps 9;
QY 568 EDLVLPWTLDLRRKLGALCTVVWSEWHEGLVAVCTLEQLTHFFVSELEFVAINK 47
DB 488 DWEETPDQITVGRIQSSEGVYKRWWRGVAVSMINVTATPQQLQAEKNEVGLR 546
QY 628 SIKRPRIYIMSAVTEFRIKIVTFVTSGLLYPLIESGVKIDETREIMAFVAKOM 607
547 KTAQVYHIFMYSYER LQIAVLTWETSESYOHRIEPLFPEMFIHLAGQIAQOM 604
DB 688 NYLRKRKDFIVRIKLESLQIVQYVAVVLEKLEFLEAPLILSS--KSAATPEWAP 745

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DB 688 NYLRKRKDFIVRIKLESLQIVQYVAVVLEKLEFLEAPLILSS--KSAATPEWAP 745
QY 746 EVLRDHSNE KSLVSPGVIIWELAHLDQWENILA LVVAAY HIRKRIILPR 77
DB 663 EVLRMCKRNYSSQSVYAFIVLYELMIGSYFNINRQGLIRVYLVYDILCKVP 177
QY 800 YVNR--LASELVAVWATFWKRSSEIMETKRMKTAH 800
DB 723 SNTFAEPFLMAKCTFFEFEPDFPQGLASTKAST 723
RESULT 10
KRAB_MOUSE
AC YEAP_MOUSE ELENVAEL 100 100 AA
DI 01 AUG 1992 (Rel. 23, Created)
DI 01 AUG 1992 (Rel. 23, Last sequence update)
DI 16 OCT 2001 (Rel. 40, Last annotation update)
DE YEAP_MOUSE protein serine/threonine protein kinase (1-23)
GN (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euprimates; Eumammalia; Eutheria; Euarchontari;
OC Mammalia; Eutheria; Eumammalia; Eutheria; Euarchontari;
OC NCBI TAXID 10090;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE 9127135; PubMed 2022997;
KA Miki T., Fleming J.P., Grossenz M., Maling M., Bump K.,
KA Reynolds S.H., Aaronson S.A.;
RT "Development of a highly efficient expression cDNA library: isolation
RT application to oncogene isolation."
RL Proc. Natl. Acad. Sci. U.S.A. 89:107-111(1992)
CC 1 FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
CC FROM THE CELL MEMBRANE TO THE NUCLEUS.
CC 1 FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC PHOSPHORYLATION
CC OF HIPPOCAMPAL NEURON.
CC 1 PHOSPHATASE PARTICIPATES IN A PHYSIOLOGICAL FEEDBACK LOOP THAT INHIBITS
CC A TIFA BRAF (T18) ONCogene OPTIMALLY EXPRESSED IN A FIBROBLAST
CC INDUCED HEPATOMA.
CC 1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MIL/RAF SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/seq/seq.htm
CC or send an email to license@isb.ch).
CC -----
DR EMBL: M64429; AAA3320.1; ALT INIT.
DR PIR: A40951; IVMSRF.
DR HSSP: P13923; LECK.
DR MOP: MGI88195; Hrat.
DR InterPro: IPR00719; Euk_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP binding; Serine/threonine-protein kinase;
KW ATP-binding; chromosomal translocation.
FT NON_TER 1 1
FT DOMAIN 19 279 PROTEIN KINASE
FT NP_BIND 2 44 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 138 148 BY SIMILARITY.
SQ SEQUENCE 328 AA; 36986 MW; 67A2E0F06A70F0C0 C0C04.

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Query Match          10.4%; Score 460; DB 1; Length 328;
Best local Similarity 39.3%; Pred. No. 4e-23;
Matches 110; Conservative 59; Mismatches 97; Indels 14; Gaps 9;

QY 568 EDLVIPWTDLDLRKLGAGSGFTVYRGWHSQSDVAVKILLTEQDFHPRVNEFLKEVAIMK 627
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
bb 10 DDWEIDPQQITVGGRIQSGSGFTVYKQKWHG-DVAVKMLNVTAPTPOOLQAFKNEVGVIK 68

QY 628 SKKHNNIVLPKNAVTRKPNLSIVLEYLSEQSLSEYELLHFSVFKLLELFRINMAFTVAKGM 687
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
bb 69 KTRHVNILLPMGYSTK-PQLAIVTQWCEGSSLYHHLLHIIETK-FEMIKLIDIAQTQAGM 126

QY 688 NYLKKRQPTIVHRLKSTFRLVLPVYIVVQVTPISPKAPTEISS--KSAASPEFHWMAP 745
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
bb 127 LYLNALSLTHPECKKRNATLHEDLTVPICPEPLATVFSFWSSGHQEQLSGSLHWMAP 184

QY 744 KVLKEDPEPNE KSVVYSNVAVILWFATIQDPQCNINPA QVVAAV--GPKGKRLDIPR 799
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
bb 185 EVIRMQDKNPYSFQSDVATAGIVLTETLMTGQLPYSHNNRQQLIFMVCEGYLSPLSKVP 244

QY 800 VVNPK-LASLIVAWADEPWFPSPSSIMETIKPMTKQAP 838
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
bb 245 SNQPKAMKRLMAECLKKKQERHLEPQILASIELLARSLEP 284

RESULT 11
RMIL_AV111
ID RMIL_AV111 STANDARD; PRT; 367 AA.
AC P10533; Q85612; Q85613; Q85614;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-MAR-2002 (rel 41, Last annotation update)
DE Serine/threonine-protein kinase transforming protein Rml1
DE (EC 2.7.1.37).
GN V-RMIL.
OS Avian retrovirus IC10.
OC Viruses; Retroviridae; Avian type C retroviruses
OX NCBI_TaxID 11874;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE-89160254; Pubmed 2537952;
RA Eychenne A., Marx M., Dezelic P., Calothy G.;
RT "Complete nucleotide sequence of IC10, a retrovirus containing the
RT Rml1 oncogene transduced in chicken neuroretina cells infected with
RT avian retrovirus RAV-1."
RL Nucleic Acids Res. 17:1250-1250(1989).
RN 121
RP SEQUENCE FROM N.A
RX MEDLINE-89091077; Pubmed 2850163;
RA Marx M., Eychenne A., Laudier D., Bechade C., Crisanti P.,
RA Dezelic P., Pessac B., Calothy G.;
RT "A novel oncogene related to c-mil is transduced in chicken
RT neuroretina cells induced to proliferate by infection with an avian
RT lymphomatosis virus."
RL EMBO J. 7:3369-3373(1988).
CC -1- CATALYTIC ACTIVITY: ATP + a protein + ADP + a phosphoprotein.
CC -2- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-R-MIL
CC POLYPROTEIN.
CC 1- SIMILARITY- BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MIL/PAF SUBFAMILY.
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or send an email to license@isb-sib.ch).
-----
CC
DR EMBL: X13744; CAA32008.1; ALI_SEQ
DR EMBL: X13438; CAA31790.1; ALI_SEQ.
DR PIR: S01645; TVFVMI.
DR HSSP: P11362; 1FGK.

```


QY	679	EMLEENLVVGGELVAVAEICLLEKAAHLLLSKKAAGTITLWMAVLVLRKLS	SNKSD	758
Db	678	RIHLKFNLLVKKYTVKIGTGLSGKAMTLLSKFLAAGTPEWMALEVERLEFSNERS	737	
QY	759	VYSGVILWELATLQOPWNIINPAVVAAGVCKEKLDPEDVNPKLASLIVACWADEPW	818	
Db	738	VYSGVILWELATLQOPWNLINPQVIAAAGVFNKRLDIPSDENPQVATLEACWANEPW	797	
QY	819	KPDSSIMPTIFPMTKQAPQQRSD	845	
Db	798	KPDSEIMDMLRPHLKSPIPPPGHTD	824	
RESULT 3				
Q9ZSD9				
ID	Q9ZSD9	PRELIMINARY	LEN	829 AA
AC	Q9ZSD9			
DT	01-MAY-1999	(TREMBLrel, 10, Created)		
DT	01-MAY-1999	(TREMBLrel, 10, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel, 19, Last annotation update)		
DE	ETHYLENE-INDUCIBLE CTRL-LIKE PROTEIN KINASE			
OS	Lycopersicon esculentum (Tomato)			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Tracheophyta; Magnoliopsida; Eudicotyledons; Core eudicots;			
OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum			
OX	NCBI_TaxID:4081			
RN	[1]			
EP	SEQUENCE FROM N.A.			
RC	STRAIN-CV, ALLISA CRAIG			
RA	Kanaan P., Giovannoni J.J.,			
RT	"Ethylene-inducible tomato CTRL-like protein kinase."			
KL	Submitt. 3 (DEC 1999) to the EMBL/Genbank/DBJ databases			
CC	1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR	EMBL: AF110518; AAD10056.1; -			
DR	HSSP: P08631; 1AD5.			
DR	InterPro: IPR000719; Fpk_kinase			
DR	InterPro: IPR002290; Ser_thr_kinase			
DR	InterPro: IPR004040; STY_kinase			
DR	InterPro: IPR001245; Tyr_kinase			
DR	Pfam: PF00069; kinase; 1.			
DR	PRINTS: PR00109; TYRKINASE			
DR	SMART: SM00221; STYK; 1.			
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.			
KW	ATP binding; Kinase, Serine/threonine-protein kinase, transferase.			
SQ	SEQUENCE 829 AA; 91889 MW; 9E976BF7640CE11D CRC64;			
Query Match				
Best local similarity 54.5%; Score 2418.5; DB 10; Length 829;				
Matches 506; Conservative 103; Mismatches 191; Indels 67; Gaps 19;				
QY	3	MGCKRSDYSLSQIPDEEVGIGASTSFYLSVAAGNVI	53	
Db	1	MSGRSSYTLNQINQNPQVADKP	54	
QY	51	GHHRMTQAYRLN	111	
Db	55	MQGLMMGSHNRVATFVVG	109	
QY	112	LDDPRVVMKAVSGSGSKSWAQTFESFQIQPI	171	
Db	107	GGSSVARNWAQTFESYQLQALAIRLSSEATCA	155	
QY	172	LRSLGTSAPAI	229	
Db	156	SRQNSPASAVTMSHRIWNGTMSVTKVTEGFYWYQMI	215	
QY	230	SLKTVSSLSSTIEVLIDHPSASIKELQNPVHNIS	289	
Db	216	SLKAVTSPKATSVFVITVETNDISKIKENKHSIS	275	

QY	290	SYSNLEDDIVSAWKRESDIDRETDLSAVIPIHLSVSLVLRPHALFEVVAISHTLGRFA	349	
Db	276	AAVAGEELVSMKSGCNGLKDRGRTIVLIGSLSVLGRHALLFEVVAITLGRFA	349	
QY	350	KCKYTRERDAESCLVRERLEPEYLLDLPDPDMLADPSLANDEFTSTSTETPFLK	409	
Db	336	KCKYTNSSDASSCLVRERERLEVILVILQKPEVSEFTSLNDEFTSTSTETPFLK	399	
QY	410	PIERTIDPESLAKQYFLDSQSLNLPVPAASNNVSVSKTAAFNVYQRI	469	
Db	396	QVEPIIDFKSLAKQYFLDSQSLNLPVPAASNNVSVSKTAAFNVYQRI	449	
QY	470	VIDPRKASGL	529	
Db	449	SSSSNPTTISLPPPTINAWKFGGRKINSLSKMYNPKS	509	
QY	522	LHFGNETVTHLLALGHFERMDVHNLFTVLEACLEK	579	
Db	503	VPPP-REDAQSPMT---	569	
QY	520	RERAGASLCTVYKGLWRGSDVAVELTDEGSEHLEAVLELEVAEMKLEHINLVLEM	609	
Db	558	MERTGAGSEFTVHRGDSVAVRILMEQDFHAERIKERLEVAIMKLEHINLVLEM	617	
QY	610	AVTEHNLSIVTHYLSRGSYLELSEFVEL	669	
Db	618	AVIQPNELIVTEYLSRGSYLELSEFVEL	677	
QY	670	RRPKSRNLLVFFVIVFV	739	
Db	678	RRLESPNLLVKKYTVKIDEGLSREKANTLSEFAACTEKMAFVIRLEFSNERS	737	
QY	764	VYSGVILWELATLQOPWNLINPQVIAAAGVFNKRLDIPSDENPQVATLEACWANEPW	818	
Db	738	VYSGVILWELATLQOPWNLINPQVIAAAGVFNKRLDIPSDENPQVATLEACWANEPW	797	
QY	819	KPDSSIMPTIFPMTKQAPQQRSD	845	
Db	798	KPDSEIMDMLRPHLKSPIPPPGHTD	824	
RESULT 4				
Q9ZSD8				
ID	Q9ZSD8	PRELIMINARY	LEN	806 AA
AC	Q9ZSD8			
DT	01-MAY-1999	(TREMBLrel, 10, Created)		
DT	01-MAY-1999	(TREMBLrel, 10, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel, 19, Last annotation update)		
DE	ETHYLENE-INDUCIBLE CTRL-LIKE PROTEIN KINASE			
OS	Lycopersicon esculentum (Tomato)			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum			
OX	NCBI_TaxID:4081			
RN	[1]			
EP	SEQUENCE FROM N.A.			
RC	STRAIN-CV, ALLISA CRAIG			
RA	Kanaan P., Giovannoni J.J.,			
RT	"Ethylene-inducible tomato CTRL-like protein kinase."			
RA	Submitted (DEC 1998) to the EMBL/Genbank/DBJ databases.			
CC	1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR	EMBL: AF110519; AAD10057.1; -			
DR	HSSP: P08631; 1AD5.			
DR	InterPro: IPR000719; Fpk_kinase			
DR	InterPro: IPR002290; Ser_thr_kinase			
DR	InterPro: IPR004040; STY_kinase			
DR	InterPro: IPR001245; Tyr_kinase			
DR	Pfam: PF00069; kinase; 1.			
DR	PRINTS: PR00109; TYRKINASE			
DR	SMART: SM00221; STYK; 1.			
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.			
DR	PROSITE: PS00109; PROTEIN_KINASE_ST; 1.			

DR PROSITE: PS00011, PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Hypothetical protein; Transferase.
SQ SGNRSTF 133 AA; 11228 MW; 9807125RIPRIR38 QPC64;

Query Match 27.6%; Score 1223; DB 10; Length 1030;
Best Local Similarity 34.9%; Pred. No. 1116-82;
Matches 314; Conservative 129; Mismatches 242; Indels 236; Gaps 21;

QY 137 ESEFQLQPIVILPSSDXTCAADPNFMOPROFA-----AFPSLSIS-----AFAISH 184
DB 139 EEENQIQ--LALFLISA-----REDP-----EATQTEALKQPSLGSCLAPENSPAELIAY 184
QY 185 REWVNCMSYLEKVPFCPLYLHGMDEPYVWSLCTNLQEDGRIPSEFIKTVDSISGSSIEV 244
DB 185 RYWNYNCLGYNKAGGCTYGLGVV-----HAGSAERITPFLLELQCTPVSDGVTEWA 236
QY 245 VLIDRHSPASIKRIGN-----EVNIISSSCVITKEVADHIAKLVCNHLGGSVSEGEDD 297
DB 247 VLVNPSSGDSNLLPIELMALDIAAKSPKSVSSSGFVNSLVPKLAITVGYMGPPVHVPE-S 295
QY 298 LVAWEKESQSLDIAKLQSAVILLESLSVGLDGRFAALLFVIAQSLITPFLARGKRYCTE 357
DB 296 MLRAWPSLSYSIKATIGSMVLPLGSLITGLAPHPAIIKFKVLGDSVTPVPRIVKGGQYTG 355
QY 356 LQAGAGGVKICLIRKLYLGLGLLKLKGLCC-----QFDELRLNLS 398
DB 356 EDVAMNFIKADIGREYIVDLMDDPGTLIPADAAGLQIDYDESAYSASPGDNDSIHVASSS 415
QY 397 LSISS-----PDR 404
DB 416 NGIESSEYENTEFTGDEHESSTKSSGEFNQSGGGGLIVHPNLSREEVKNQKVEKAPFQ 475
QY 466 LRLKGLLFLHLEALA-----KQYFLSSGSLN LAFDEASSG 441
DB 476 NLSSRPILHSFTMRSPSWIEGVSSPAAQRMKVKQVDSQYMLDAAKENFRLAKLHDVLLES 535
QY 442 NVVSGKDAAFSVYQRP-----NPKVDVQKTIIVT-----AAQINTED 492
DB 536 GVVAPPNLFSEVYPQGLEAIVESKNSTFAFECEKGLITTPGCRHNGFGVFFLPLPF 595
QY 472 GPKDENSELAKER-----NPKVDVQKTIIVT-----AAQINTED 492
DB 596 VQSKTNAHQKQNGKVVQSQSDSSHSEASSTEYARTVPAAVAAAVVASSMVAASAAKSAN 655
QY 493 QKSLQPKSCVAASYVQSITIVENVVTLSEHLSILQS-EDSEHILLALSHPMDHVNMLPFV 551
DB 656 SDSSPIELPAAAAATAATAAAVVAATAAAVSRQLELGSNSDGDGSGGHHFQSGSDSN 711
QY 654 HGSQLEKKEK-----LSSLL-----GAVITWTLFLFFPLAGSEGTIVYFS 534
DB 712 HG-----PNSGGERISDKSLGNSLSSKSLGGLVSLCEILWEEITVGERIGLSYGEVYRG 765
QY 695 EWHGSDVAVKILTEQDFHPDPRVNEFLREVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYL 654
DB 766 DWIGTEVAVKRPDQQLIGALELLEKSEVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYL 825
QY 885 SKESLYKLLRSQVRLDITLPIETPMALIVAKGMNYLHRELPPIVHIDLSKNLIVDKKYT 714
DB 826 PROSLYRLTHRPN NQIDERRRLRNALDAARGMNYLHSONPMIVHRLDKSPNLLVDKNWV 884
QY 917 YKVTLPLSSAFSTTTPPEFAATTEWNAETVLEPFTENFFGVVSYSPVILWELATLQQ 774
DB 885 YKVDGFLSRMKHSTYLSKSTAGLAEMWMAPEVLRNEPADEKQDVSYGVILWELFTLQQ 944
QY 775 PWNLNPAQVVAAGVQKCELDIPQVNVNPKIASLIVACWADPEKWRKPSSTIMFTLKPMFT 834
DB 945 PWCKMNPQVVGAVGQHEPRLDIPQVNDPAIANLSKCWQDTSKLRPSFAEIMASIKRLQ 1004
QY 835 K 835
DB 1005 K 1005

RESULT 9
Q9FRR5
IN Q9FRR5 PRELIMINARY; 1997; 2651 AA.
AC Q9FRR5;
DT 01-MAR-2001 (TrEMBLrel. 16; Created)
DT 01-MAR-2001 (TrEMBLrel. 16; Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19; Last annotation update)
DE F22013.20;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID:3702;
RN 111
RF SEQUENCE FROM N.A.
RA Khan S., Brooks S., Buchler E., Chao Q., Johnson-Hopson J., Kim C.,
RA Shinn P., Altati H., Bei Q., Chin C., Chien J., Choi E., Goun L.,
RA Conway A., Gonzales A., Hansen N., Hownd B., Koo T., Lam B., Lee J.,
RA Leuz G., Li J., Liu A., Liu K., Liu S., Mukharzky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Tsimi M., Vaysberg M., Yu C., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RF Genomic sequence for Arabidopsis thaliana BAC F22013 from chromosome
RT 1.;
FI Subunit 1 (TAN-2001) to the ENR GeneBank (DBJ) databases.
DE EMBL: AC003981; AAF99762.1;
DE HSSP: P08799; 1MND;
DE InterPro: IPR002710; DIL;
DE InterPro: IPR000719; Euk_pkinase;
DE InterPro: IPR000048; IQ;
DE InterPro: IPR01609; myosin_head;
DE InterPro: IPR004009; Myosin_N;
DE InterPro: IPR022990; Ser_thr_pkinase;
DE InterPro: IPR004040; STY_pkinase;
DE InterPro: IPR001245; Tyr_pkinase;
DE Pfam: PF01843; DIL; 1;
DE Pfam: PF00612; IQ; 6;
DE Pfam: PF00063; myosin_head; 2;
DE Pfam: PF02726; myosin_N; 1;
DE Pfam: PF00069; pkinase; 1;
DE PRINTS: PR00193; MYOSINHEAVY;
DE PRINTS: PR00109; TYRKINASE;
DE ProDom: PD000355; myosin_head; 1;
DE ProDom: PD003376; DIL; 1;
DE SMART: SM00015; IQ; 6;
DE SMART: SM00242; MYSC; 1;
DE SMART: SM00221; STYK; 1;
DE SMART: SM00220; S_TK; 1;
DE SMART: SM00219; TYRK; 1;
DE PROSITE: PS00011; PROTEIN_KINASE_DOM; 1;
KW ATP-binding; Transferase.
SQ SEQUENCE 2651 AA; 298991 MW; 1352A42849R9RHSV QPC04;

Query Match 27.5%; Score 1220; DB 10; Length 2651;
Best Local Similarity 33.7%; Pred. No. 816-82;
Matches 315; Conservative 129; Mismatches 276; Indels 216; Gaps 21;

QY 86 SSELSSVYVYAPLEENPAANEINALEYILDDPRVMEAVGSDSSSEKSWAGLHESQIQQL 141
DB 139 SSMASEP-AFLAASNEADYMSSE PFFVQVCLALALANASGSE SFLLEPFLAA 189
QY 146 LVLRISSEXTCAEDPNEMOPIPEALALNGLSLSAFALSHEFVWVWQPMALIKVDPGYLI 205
DB 190 TLLSLGSHQR-----MDSRRD-----SSEVVAQLSKQVWEYGVLDYERKVVSEFY 260
QY 205 HCMFPYVWSLCTNLQETGPIPSFESEKTVFASLGSSIEVVLIRLRSWAKLKLQKRVHNI 265
DB 236 -----DVYSLSDSAKQGEPSLESDLESNHGTGQ--FEAVVWVNRPIIDSSSHLELLEIA 288
QY 266 SSSSAVIT--KEVADHIAKLVCNHLGGSVSGQWIMVSAWKEPSTDLKKEQLDASAVIPLASL 325
DB 289 ALGQSTTSVSVLVQPLAFIVTFPMQPS-AFNSIVLAPWTERKSSSEKKAALNTVFFPLGV 347

QY 451 YLE LKELVGEKIVVTLELENSALLAKKA 122
DB 419 PAFEDPKNATESIKSSIAFKGINNENSDFRFRRENVVPPSAPSQPLVYKNWSACNDISN 478
QY 486 AQENTQFCKFFPFGCVASPYVQSITFEV----- 515
DB 479 NKQYNVAIGSVPRFNATNASSSQAISTAKHYN----PNVPFLNPMYAAPNPDNFI 534
QY 516 -----NVVPLSHSHIGSED----- 530
DB 535 IGTSAMAKASTGNCIDRSQVPPGILYDKMIGTSSMNTASSSGIGKVAEKDLQNDLEKGP1 594
QY 531 -----SEHLLALSHPRMDHVNLD-----PFVHGSQLIR-----KPN 561
DB 595 YSRFAGELSKNAQGFPERDRKENGCSYDHRMLHPDPRKSPIDRPMRPRQNIQCVSPS 654
QY 562 ELSLGLRLV-----IPWTDLRLKIGAGSEGTVYRGEGHGSIDVAVKILTEQDFHP 613
DB 655 QVGSCKVDLVDEVSECEILLWEDLVIDERIGISYGEVYHADWNGTEVAVKKFLDQEFYG 714
QY 614 ERVNEFLREVAIMKSLRHPNIVLFMGCAVIKPPNLSIVTEYLSRGSLYRLHKSGVKDIDE 673
DB 715 DALEEFRCFVRIMRPLRHPNIVLFMGCAVLEPPLHSIVSEYLFKSSLYKLIHRPNCQ-IDE 773
QY 674 TPRINMAFDVAKGMNLYLHRDPPPIVHEDLKSPNLLVDKKYTVKVCDFGLSRLKARTFLSS 733
DB 774 KRRIKMAIDVARGMNCILHTSVPTIVHRDLKSPNLLVDNNVTWKVCDFGLSRLKHSSTFLSS 833
QY 734 KSAAGTPENMAPEVLRDEPSNEKSDVYSFGVILWELATLQQPWCNLPNPAQVVAAGVGRK 793
DB 834 KSTAGTPENMAPEVLRNEQSNKCDIYSEFGVILWELATIRKPPWHGMNQMVVGAVGEQDR 893
QY 794 RLDIPRDVNPKLASLIVACWADEPWKRPSFSIMETLKPMTKQADPOOSRT 844
DB 894 RLDIPKEVDPIVASIIRDCWOKDPNLRPSFIQLTSYLKTLQIRLVIPSHOET 944
RESID 14
Q9LM32
ID Q9LM32 PEELEMINIAEF FET 983 AA
AC Q9LM32
DE 01-OCT-2000 (TrEMBLrel 15, Genat 1)
DI 01-OCT-2000 (TrEMBLrel 15, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel 19, Last annotation update)
DE 110022.13
OC Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Eudicotyledons; Eucomidiales; Fagiales;
OC Eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX MBI_Pax1P 2702.
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Boehler E., Chao Q., Johnson Heggson C., Khan S.,
RA Kim C., Altati H., Bel Q., Chen C., Chien J., Choi E., Cobb L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo P., Lam B., Lee J.,
RA Luo Z., Li J., Liu A., Liu K., Liu S., Mukharevy N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Weaver A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.
RT "Genomic sequence for Arabidopsis thaliana BAC T10022 from chromosome
RT 1".
FC Submitted (JUN 2002) to the International Protein Databases
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR FMBL: AC069551; AAF78731; ...
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kinase
DR InterPro: IPR004040; STV_pkinase.
DR InterPro: IPR001245; Ty_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00221; STYKQ; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_FOM; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW All readon, Serine/threonine protein kinase; Transferrase.
SQ SEQUENCE 988 AA; 107398 MW; 8D40755955B96F81 (CDS);
Query Match 23.8%; Score 1057.5; DB 10; Length 988;
Best Local Similarity 30.3%; Pred. No. 70;
Matches 315; Conservative 129; Mismatches 288; Indels 309; Gaps 64;
QY 36 GGNVIRGRTDRVFDWVGSGDRI-----NTQAVRIGNIYSWIGIQHHSSSSSYDSSSLSS 90
DB 22 GEGSVSNRKNESLAELSLIDSLSSGQNSLEKPLDLSNKKLAVYHDESLISQNAKREK 81
QY 91 EYVAPILSNPAAINEINALEYILDDERVMKAVGSG-----GSSGSKSWAQTEESFQLQQL 146
DB 82 DEETHHGGCVQSE-----FQMGGCLGFTREDFEVEEYQIQ- 112
QY 117 VRLGGGWTCAQETNMDFHDA ALKGLD-----AMALCHETWVY 174
DB 121 ALLESA REDI PAAQIHAKQFGLAGRI SAPDNTDAHMAYNWYNPL 168
QY 193 SYLFFVPEETFLHPMPYVWSLTNIGEDS-PIPSPESEFVSSDSSFLVVIIRH 258
DB 169 GYDKIVNGFY - DLSGVNNSSELEKPLTAVDQGLVGVHVIWIAVIVNSS 218
QY 251 SPASLKELENEVHNI -SSSAVITKIVANHIAKLVNHIAHNVVDEHILYSARK 303
DB 219 KDSMLLELPQMALDIAAKKFASSGSPVNSHIVELAVIVAPYMSGVLD PWTIRAKW 272
QY 304 EGSNDLKEGLSAAVPLCSLSVLECPHALLFKVLAQSDLPDPIAKGPKYTRIDAS- 361
DB 278 SLSSYSLKATLPSMVLPGLSLTIGLAPHALLFKVLAQSDVAVTRVKEVYLSGSTVAMN 357
QY 362 -----SCLVRFGLD-----REYLLDLGRPCGLQPDSE-ENGLSSSLSSSP 402
DB 338 SIKEDGSGCKL-FSLINPNVNPEYIVDMGDPATLIPAPAAGLQMEHDSVYSASPRIV 399
QY 403 -----LRFKLD----- 408
DB 397 ESSHVASSGSGVSECHHTTSWGAHHEFTZETREHRLSALNNIMLREHAYLLEA 459
QY 409 - FLPESLIDKSLA- KLLTGG- NQGNVAVGLA 460
DB 427 FVCHLASEFTREFTARESTSWTEVYSAFLAHREVEV-VEHRLAARIMSLAQRIDHVL 419
QY 439 SSCNVVSGKDAALSVYQFELNRKIVCKIIVVLEKTRNSQLNDEKAAINLQKESK 490
DB 517 LSGVVAPENLSEVY -SSSMNAGELEKVALNKKERKIVLQGNQGS 509
QY 497 QFFSVAATYSVQETTV ERVVLVLIJH -LEHLEHLELALHLEHLEH 549
DB 567 KLSIVSELIIFKPKQSEATTHLLEHSSGSLCHLCHGRVGDHNSAB -SLSSGID 542
QY 546 NNLP-----FVHGSQLI----- 559
DB 623 ENVTVAVAAMAAVVASGMVAAAKZANFETLLELAMAAMAAVDELMVHAFHMLAN 682
QY 558 -----RKPNELSLDP-----DLYVFWLLEHLEHLEHLEH 599
DB 683 GDAAGSGULRGVDGGERISDRSTGNSSKSDAAIDDAEVELLWREELIVAKRIGIGCSI 742
QY 591 VYGEWHLEFTV AVFILLTQGFHPEFVNLEFEVAIMKSLLEHNVLMVAETFEHLEST 649
DB 743 -LAVLSATLVMAVEKFLDGLDGLAALH- 789
QY 650 VTEYLKSGELYRLHKSGVREHLEPKINMAIVAKGMNAQSSSDLVKRGKGNILV 709
DB 784 VTETLPQGSIVELTHFPN NQIDPPKPMKMAIQAAMQVYHSHNVYHDEKSPRLV 842
QY 719 LKKYIVKVLLEGLSFLAARHLSKSKAAAGLLHMAILEVLEHLEHLEHLEHLEH 769
DB 843 DKNWVVKVCDPGLSRMKVSYLSSKSLAGIARWMAPEVLRNEPADAQTLVSYGVILWEL 902
QY 779 ATLLQCPWNI NPAQVVAAVVPEKPEFLTPFVVDVYASLIVAVWALHLEHLEHLEHLEH 829


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Db 545 DTPWGLNKKKAGSGFVURAEWHGSDVAVKILMEQDPHAERVNEFLREVALMKRLR 604
QY 545 HPNIVLFMGAVTKFNNLSIVTEYLSKGSYKLLHKSQVKD-IDETKRINMAFDVAKGMNY 689
Db 605 HPNIVLFMGAVTQPNLSIVIEYLSRGSLEYELHKSQARFOLDERRLSMAYDVAKGMNY 664
QY 690 THRRDDPIVHDDIKSPNIVDKKYTVKVGDFGLSLKARTFLESSKSACTFEWKAPEVLR 749
Db 665 THRRNETVIRKDLKSPNIVDKKYTVFVGFGLSLKASIFLSSKSAAGTPEWMAPEVLR 724
QY 750 DEPSNEKSDVYSGVILWELATLQOPWGNLNPACVVAAGVFGKGRILDIPRDVNEKSLASLI 809
Db 725 DEPSNEKSDVYSGVILWELATLQOPWGNLNPACVVAAGVFGKGRLEIPRNLNQVAAII 784
QY 810 VACWADEPWKRPSFSSIMETKPMTKQAPPOQSRID 845
Db 785 EGVWNEPWKRPPSPATIMDLRLPLIKSAVTFPNRSD 820
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RESULT 3

```
US 08 261-432-2
Sequence 2, Application US/08261432
Patent No. 5602422
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5602322ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
```

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08261432

FILING DATE: June 17, 1994

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/003,311

FILING DATE: January 12, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Lori Y. Beardsell

REGISTRATION NUMBER: 34,293

REFERENCE/DOCKET NUMBER: UFN-1864

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 821 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US 08-261-432-2

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Query Match 61.8% Score 2742.5; DB 1; Length 821.
Best local similarity 62.3%; Pred. No. 2.4e-237;
Matches 546; Conservative 99; Mismatches 144; Indels 87; Gaps 14;
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QY 1 MEMPGRRSDYSLASQIPDEVG---TGASTSFYDSVAA-----CGNVIKGPTDR-VFD 49
Db 1 MEMPGRRSNYTLSSQFSDQVSVSVIGAPPHPHYDLSSENKSNHNSGNTGKAKAERGQFD 60
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QY 50 WQ---QDNDNNTQAVRIG NLY GVLMLLEBAAVTVVLAAGVATATLSNAAAN 100
Db 61 WQSDGNDGNDNNTQAVRIG NLY GVLMLLEBAAVTVVLAAGVATATLSNAAAN 100
QY 104 EINALTYILDDPRV-----MKAVGSRC-SSQKSWAQGLESEGLQDPIVRL 100
Db 120 EIESVGFDDIDGPRV-----MKAVGSRC-SSQKSWAQGLESEGLQDPIVRL 100
QY 151 SSGXICADNNDMDPIETMAALKGLTLEADLSHRIWVNAQBNYLERVNTATYLRMDP 21
Db 180 SSGXICADNNDMDPIETMAALKGLTLEADLSHRIWVNAQBNYLERVNTATYLRMDP 21
QY 211 YVWSLCTNIQDMPIDPSPELEKTVPSGLDFTLVVLTRESDASRLKRLKRVVRISSSV 21
Db 240 YVWSLCTNIQDMPIDPSPELEKTVPSGLDFTLVVLTRESDASRLKRLKRVVRISSSV 21
QY 271 TTPVAVADHAKLVGNHLCSSVSGEGLDVSARERLSEGLKRLKRVVRISSSV 21
Db 300 TTPVAVADHAKLVGNHLCSSVSGEGLDVSARERLSEGLKRLKRVVRISSSV 21
QY 331 KALLKVLADSDIDPCRIAGCKYCIKIDASSLVKFGDKRYLGLDGRGGLQDPIVRL 300
Db 359 KALLKVLADSDIDPCRIAGCKYCIKIDASSLVKFGDKRYLGLDGRGGLQDPIVRL 300
QY 391 LMGDSICISDPIPPDPIKPIESTIDDPDIAKAVDIDGSPNINIVTASRVVAVRIAA 400
Db 419 LMGDSICISDPIPPDPIKPIESTIDDPDIAKAVDIDGSPNINIVTASRVVAVRIAA 400
QY 451 EGVVLEDFDPRFVATFTIVVLEKESL---GVAAQLKSLKSLKSLKSLKSLKSL 400
Db 472 EGVVLEDFDPRFVATFTIVVLEKESL---GVAAQLKSLKSLKSLKSLKSLKSL 400
QY 511 TPVFNVVPLSHISHIGSEDSERHLLSHRMDHVNINIPVHNSLIRKDNLSLALRI 500
Db 497 TPVFNVVPLSHISHIGSEDSERHLLSHRMDHVNINIPVHNSLIRKDNLSLALRI 500
QY 571 VTPWTDIIPKICAGSPQTVYPCGEWIRGSIWAVKILTEZTHIRVWVLELREVALEKSR 600
Db 545 DTPWGLNKKKAGSGFVURAEWHGSDVAVKILMEQDPHAERVNEFLREVALMKRLR 604
QY 631 HPNIVLFMGAVTKFNNLSIVTEYLSKGSYKLLHKSQVKD-IDETKRINMAFDVAKGMNY 689
Db 605 HPNIVLFMGAVTQPNLSIVIEYLSRGSLEYELHKSQARFOLDERRLSMAYDVAKGMNY 664
QY 690 THRRDDPIVHDDIKSPNIVDKKYTVKVGDFGLSLKARTFLESSKSACTFEWKAPEVLR 749
Db 665 THRRNETVIRKDLKSPNIVDKKYTVFVGFGLSLKASIFLSSKSAAGTPEWMAPEVLR 724
QY 750 DEPSNEKSDVYSGVILWELATLQOPWGNLNPACVVAAGVFGKGRILDIPRDVNEKSLASLI 809
Db 725 DEPSNEKSDVYSGVILWELATLQOPWGNLNPACVVAAGVFGKGRLEIPRNLNQVAAII 784
QY 810 VACWADEPWKRPSFSSIMETKPMTKQAPPOQSRID 845
Db 785 EGVWNEPWKRPPSPATIMDLRLPLIKSAVTFPNRSD 820
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RESULT 4

PCT-US93-07347-2

Sequence 2, Application PC/TUS9307347

GENERAL INFORMATION:

APPLICANT: Ecker, Joseph R.

APPLICANT: Kieber, Joseph J.

TITLE OF INVENTION: Constitutive Triple Response Gene and

Mutations

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and

ADDRESSEE: Norris

STREET: One Liberty Place 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

Best Local Similarity 40.9%; Score 504.5; DB 4; Length 455;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;
QY 564 SLGLEDLVLPWTDLRLKIGAGSFGTVYGEWHGSD--VAVKIIITEQDHPERVNEFLR 621
DB 3 SLGASPVQIKFDLQFFENCAGSGSVYFAKWISQKKEVAVKLLKIE-----K 52
QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTFYLSRGSLSYLLHKSQVVDIPETPPINMAP 621
DB 53 EAEILSVLSHRNLIQFYGVILEPPNYGIVTEYASLSGLSDYDINSRSEEMDMDHIMTWAT 112
QY 682 DVAKGMNYLHRRDP-PIVHRDLKSPNLLVDKKYTVKVCDFGLSRKARTFLSSKSAAGTP 740
DB 113 DVAKGMHYLHMEAPVKEVILHRELSKNVVIADGVKICDFGASRFHNHT--THMSLVGTF 170
QY 741 EWMAPEVLHRRDP-PIVHRDLKSPNLLVDKKYTVKVCDFGLSRKARTFLSSKSAAGTP 800
DB 171 PWMAPEVIQSLPVSFETCDYSGVVLWEMLTREVPFKGLEGLQVAVLVVEKNERLTIPSS 230
QY 801 VNPKLASLIVACWADEPWKRPSFSSIMETLKPM 834
DB 231 CPRSFAELLHQCWEADAKKRPSFKQIISLESMS 264

RESULT 12
US-09-221-416-5
Query Match 11.4%; Score 504.5; DB 4; Length 455;
Best Local Similarity 40.9%; Pred. No. 8.4e-37;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;
GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/221-416
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-221-416-5

Query Match 11.4%; Score 504.5; DB 4; Length 455;
Best Local Similarity 40.9%; Pred. No. 8.4e-37;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;
QY 564 SLGLEDLVLPWTDLRLKIGAGSFGTVYGEWHGSD--VAVKIIITEQDHPERVNEFLR 621
DB 3 SLGASPVQIKFDLQFFENCAGSGSVYFAKWISQKKEVAVKLLKIE-----K 52
QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTFYLSRGSLSYLLHKSQVVDIPETPPINMAP 681
DB 53 EAEILSVLSHRNLIQFYGVILEPPNYGIVTEYASLSGLSDYDINSRSEEMDMDHIMTWAT 112
QY 682 DVAKGMNYLHRRDP-PIVHRDLKSPNLLVDKKYTVKVCDFGLSRKARTFLSSKSAAGTP 740
DB 113 DVAKGMHYLHMEAPVKEVILHRELSKNVVIADGVKICDFGASRFHNHT--THMSLVGTF 170
QY 741 EWMAPEVLHRRDP-PIVHRDLKSPNLLVDKKYTVKVCDFGLSRKARTFLSSKSAAGTP 800
DB 171 PWMAPEVIQSLPVSFETCDYSGVVLWEMLTREVPFKGLEGLQVAVLVVEKNERLTIPSS 230
QY 801 VNPKLASLIVACWADEPWKRPSFSSIMETLKPM 834
DB 231 CPRSFAELLHQCWEADAKKRPSFKQIISLESMS 264

RESULT 13
US-09-221-245-5
Query Match 11.4%; Score 504.5; DB 4; Length 455;
Best Local Similarity 40.9%; Pred. No. 8.4e-37;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;
GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/221-245
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-221-245-5

GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/221-245
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-221-245-5

Query Match 11.4%; Score 504.5; DB 4; Length 455;
Best Local Similarity 40.9%; Pred. No. 8.4e-37;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;
QY 564 SLGLEDLVLPWTDLRLKIGAGSFGTVYGEWHGSD--VAVKIIITEQDHPERVNEFLR 621
DB 3 SLGASPVQIKFDLQFFENCAGSGSVYFAKWISQKKEVAVKLLKIE-----K 52
QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTFYLSRGSLSYLLHKSQVVDIPETPPINMAP 681
DB 53 EAEILSVLSHRNLIQFYGVILEPPNYGIVTEYASLSGLSDYDINSRSEEMDMDHIMTWAT 112
QY 682 DVAKGMNYLHRRDP-PIVHRDLKSPNLLVDKKYTVKVCDFGLSRKARTFLSSKSAAGTP 740
DB 113 DVAKGMHYLHMEAPVKEVILHRELSKNVVIADGVKICDFGASRFHNHT--THMSLVGTF 170
QY 741 EWMAPEVLHRRDP-PIVHRDLKSPNLLVDKKYTVKVCDFGLSRKARTFLSSKSAAGTP 800
DB 171 PWMAPEVIQSLPVSFETCDYSGVVLWEMLTREVPFKGLEGLQVAVLVVEKNERLTIPSS 230
QY 801 VNPKLASLIVACWADEPWKRPSFSSIMETLKPM 834
DB 231 CPRSFAELLHQCWEADAKKRPSFKQIISLESMS 264

RESULT 14
US-09-163-115-5
Query Match 11.4%; Score 504.5; DB 4; Length 455;
Best Local Similarity 40.9%; Pred. No. 8.4e-37;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;
GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/163,115A
CURRENT FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-163-115-5

Query Match 11.4%; Score 504.5; DB 4; Length 455;
Best Local Similarity 40.9%; Pred. No. 8.4e-37;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;
QY 564 SLGLEDLVLPWTDLRLKIGAGSFGTVYGEWHGSD--VAVKIIITEQDHPERVNEFLR 621
DB 3 SLGASPVQIKFDLQFFENCAGSGSVYFAKWISQKKEVAVKLLKIE-----K 52
QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTFYLSRGSLSYLLHKSQVVDIPETPPINMAP 681
DB 53 EAEILSVLSHRNLIQFYGVILEPPNYGIVTEYASLSGLSDYDINSRSEEMDMDHIMTWAT 112
QY 682 DVAKGMNYLHRRDP-PIVHRDLKSPNLLVDKKYTVKVCDFGLSRKARTFLSSKSAAGTP 740
DB 113 DVAKGMHYLHMEAPVKEVILHRELSKNVVIADGVKICDFGASRFHNHT--THMSLVGTF 170

